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[illegible][illegible][illegible]

CURRICULUM	94.98	Scores 6: 4B 4; Legend 4: 2B
Test Local Similarity	0.79	Pred N: 0.00047
Matches	1	Matches 0: 100% 0: 24ps 0:
AVSETQ.MIND.1.		
AVSETQ.MIND.2.		
AVSETQ.MIND.3.		

US 09-468,417 A1

***GENERAL INFORMATION:**

APPLICANT: BARDET, Jean-Rene
INVENTOR: Barlet, Jean-Rene
ATTORNEY: Whittick, James E.
ADDRESS: Whittick, Gordon E.,
FIRM OF INVENTORS: KARATHAKI,
FIRM OF ATTORNEYS: Castropelo,
TITLE REFERENCE: 1068-1B
SERIES AND CLASSIFICATION NUMBER: 15, 230, 813
SUBJECT FILING DATE: 1999-09-04
CLASSIFICATION NUMBER: 237, 133
OTHER FILING DATE: 1997-08-01
NUMBER OF SEQUENCES: 9
SOFTWARE Patent In Ver.: 2.0
SEQUENCE NO.:
LENGTH: 28
TYPE: FBI
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Cyclic lysyl, -arg, cyclic Glut-Lys 26, and this sequence has an amino group at terminus (NH2).

Query Match	94.9%	DP 4	Length 20
Percent Similarity	91.7%	Gap 0.00047	
Matches	11	Mismatches	0
		Indels	0
Query	1	AVSETQUMINAC	12
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7
 RESULT 4-6-813-4
 1. Sequence 4, Application 05/03406810
 2. Patent No. 6116410
 3. GENERAL INFORMATION:
 4. APPLICANT: Barthel, Jean Rene
 5. ATTORNEY: Morley, Paul
 6. ASSISTANT: Whitfield, James E.
 7. ADDRESS: 10000 W. 13th, Lakewood, Colorado
 8. TITLE OF INVENTION: LAKAETHRACETAMINE ANALOGUES
 9. TITLE OF INVENTION: LAKAETHRACETAMINE ANALOGUES
 10. FILING NUMBER: 10688-1B
 11. CURRENT APPLICATION NUMBER: 317 9736 813
 12. FILING DATE: 1999-09-24
 13. PUBLICATION NUMBER: 68/961,706
 14. PUBLICATION DATE: 1997-08-01
 15. NUMBER OF SEQ. NO.: 9
 16. SOFTWARE: Patent In Ver. 2.0
 17. SEQ. ID NO.: 4
 18. LENGTH: 29
 19. TYPE: FBI
 20. FORMAT: Base Saptors
 21. FILED:
 22. FILE INFORMATION: File 6022 in 29 and this sequence has an
 23. OTHER INFORMATION: using group 1 sequences (NID).
 24. 4-6-813-4

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Query Match          94.58%   100's 6; DP 4; Length 29;
Best local similarity 91.78%   100's 6; 0-0049;
Matches 11; Conservative 0; Indels 0; Gaps 0;

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page 8
 25 x 26.2 = 655.5
 Students' Application 11/3/2024



1. $\mathcal{A} \in \mathcal{A}_n$ is a $(n-1)$ -ary complete \mathcal{A} -algebra.

Method	Sequence	Size	Time	Space	Search Time	1st Records (without additions)
1	1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100	100	0.000000	0.000000	0.000000	0.000000

[illegible]

searched: 24548, 44254, 45448, 45449, 45450, 45451, 45452, 45453, 45454, 45455, 45456, 45457, 45458, 45459, 45460, 45461, 45462, 45463, 45464, 45465, 45466, 45467, 45468, 45469, 45470, 45471, 45472, 45473, 45474, 45475, 45476, 45477, 45478, 45479, 45480, 45481, 45482, 45483, 45484, 45485, 45486, 45487, 45488, 45489, 45490, 45491, 45492, 45493, 45494, 45495, 45496, 45497, 45498, 45499, 45500, 45501, 45502, 45503, 45504, 45505, 45506, 45507, 45508, 45509, 45510, 45511, 45512, 45513, 45514, 45515, 45516, 45517, 45518, 45519, 45520, 45521, 45522, 45523, 45524, 45525, 45526, 45527, 45528, 45529, 45530, 45531, 45532, 45533, 45534, 45535, 45536, 45537, 45538, 45539, 45540, 45541, 45542, 45543, 45544, 45545, 45546, 45547, 45548, 45549, 45550, 45551, 45552, 45553, 45554, 45555, 45556, 45557, 45558, 45559, 45560, 45561, 45562, 45563, 45564, 45565, 45566, 45567, 45568, 45569, 45570, 45571, 45572, 45573, 45574, 45575, 45576, 45577, 45578, 45579, 45580, 45581, 45582, 45583, 45584, 45585, 45586, 45587, 45588, 45589, 45590, 45591, 45592, 45593, 45594, 45595, 45596, 45597, 45598, 45599, 45600, 45601, 45602, 45603, 45604, 45605, 45606, 45607, 45608, 45609, 45610, 45611, 45612, 45613, 45614, 45615, 45616, 45617, 45618, 45619, 45620, 45621, 45622, 45623, 45624, 45625, 45626, 45627, 45628, 45629, 45630, 45631, 45632, 45633, 45634, 45635, 45636, 45637, 45638, 45639, 45640, 45641, 45642, 45643, 45644, 45645, 45646, 45647, 45648, 45649, 45650, 45651, 45652, 45653, 45654, 45655, 45656, 45657, 45658, 45659, 45660, 45661, 45662, 45663, 45664, 45665, 45666, 45667, 45668, 45669, 45670, 45671, 45672, 45673, 45674, 45675, 45676, 45677, 45678, 45679, 45680, 45681, 45682, 45683, 45684, 45685, 45686, 45687, 45688, 45689, 45690, 45691, 45692, 45693, 45694, 45695, 45696, 45697, 45698, 45699, 45700, 45701, 45702, 45703, 45704, 45705, 45706, 45707, 45708, 45709, 45710, 45711, 45712, 45713, 45714, 45715, 45716, 45717, 45718, 45719, 45720, 45721, 45722, 45723, 45724, 45725, 45726, 45727, 45728, 45729, 45730, 45731, 45732, 45733, 45734, 45735, 45736, 45737, 45738, 45739, 45740, 45741, 45742, 45743, 45744, 45745, 45746, 45747, 45748, 45749, 45750, 45751, 45752, 45753, 45754, 45755, 45756, 45757, 45758, 45759, 45760, 45761, 45762, 45763, 45764, 45765, 45766, 45767, 45768, 45769, 45770, 45771, 45772, 45773, 45774, 45775, 45776, 45777, 45778, 45779, 45780, 45781, 45782, 45783, 45784, 45785, 45786, 45787, 45788, 45789, 45790, 45791, 45792, 45793, 45794, 45795, 45796, 45797, 45798, 45799, 45800, 45801, 45802, 45803, 45804, 45805, 45806, 45807, 45808, 45809, 45810, 45811, 45812, 45813, 45814, 45815, 45816, 45817, 45818, 45819, 45820, 45821, 45822, 45823, 45824, 45825, 45826, 45827, 45828, 45829, 45830, 45831, 45832, 45833, 45834, 45835, 45836, 45837, 45838, 45839, 45840, 45841, 45842, 45843, 45844, 45845, 45846, 45847, 45848, 45849, 45850, 45851, 45852, 45853, 45854, 45855, 45856, 45857, 45858, 45859, 45860, 45861, 45862, 45863, 45864, 45865, 45866, 45867, 45868, 45869, 45870, 45871, 45872, 45873, 45874, 45875, 45876, 45877, 45878, 45879, 45880, 45881, 45882, 45883, 45884, 45885, 45886, 45887, 45888, 45889, 45890, 45891, 45892, 45893, 45894, 45895, 45896, 45897, 45898, 45899, 45900, 45901, 45902, 45903, 45904, 45905, 45906, 45907, 45908, 45909, 45910, 45911, 45912, 45913, 45914, 45915, 45916, 45917, 45918, 45919, 45920, 45921, 45922, 45923, 45924, 45925, 45926, 45927, 45928, 45929, 45930, 45931, 45932, 45933, 45934, 45935, 45936, 45937, 45938, 45939, 45940, 45941, 45942, 45943, 45944, 45945, 45946, 45947, 45948, 45949, 45950, 45951, 45952, 45953, 45954, 45955, 45956, 45957, 45958, 45959, 45960, 45961, 45962, 45963, 45964, 45965, 45966, 45967, 45968, 45969, 45970, 45971, 45972, 45973, 45974, 45975, 45976, 45977, 45978, 45979, 45980, 45981, 45982, 45983, 45984, 45985, 45986, 45987, 45988, 45989, 45990, 45991, 45992, 45993, 45994, 45995, 45996, 45997, 45998, 45999, 46000, 46001, 46002, 46003, 46004, 46005, 46006, 46007, 46008, 46009, 46010, 46011, 46012, 46013, 46014, 46015, 46016, 46017, 46018, 46019, 46020, 46021, 46022, 46023, 46024, 46025, 46026, 46027, 46028, 46029, 46

1. *Introduction* 1

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[illegible][illegible][illegible]

Figure 1. Schematic representation of the experimental design. The subjects were divided into two groups: the control group (n = 10) and the experimental group (n = 10). The control group received a standard diet (SD) and the experimental group received a high-fat diet (HFD). The subjects were divided into two groups: the control group (n = 10) and the experimental group (n = 10). The control group received a standard diet (SD) and the experimental group received a high-fat diet (HFD). The subjects were divided into two groups: the control group (n = 10) and the experimental group (n = 10). The control group received a standard diet (SD) and the experimental group received a high-fat diet (HFD).

Pred. No. is the number in S.I. predicted by chance.

and is denoted by \mathcal{D}_α . For $\alpha \in \mathbb{R}$, the fractional Laplacian $(-\Delta)^\alpha$ is defined as the Fourier multiplier

STAYING

1. $\frac{1}{2} \log \frac{1}{2}$

[illegible][illegible]

1. *Phragmites australis* (Cav.) Trin. ex Steud.

2	ϵ_2	$[\epsilon_1, \epsilon_2]$	ϵ_1	ϵ_2	ϵ_1	ϵ_2
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2	2	2	2	2	2	2
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4	4	4	4	4	4	4
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7	7	7	7	7	7	7
8	8	8	8	8	8	8
9	9	9	9	9	9	9
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[illegible]

Case	Model	Method	Results
1	Model 1	Method 1	Results 1
2	Model 2	Method 2	Results 2
3	Model 3	Method 3	Results 3
4	Model 4	Method 4	Results 4
5	Model 5	Method 5	Results 5
6	Model 6	Method 6	Results 6
7	Model 7	Method 7	Results 7
8	Model 8	Method 8	Results 8
9	Model 9	Method 9	Results 9
10	Model 10	Method 10	Results 10
11	Model 11	Method 11	Results 11
12	Model 12	Method 12	Results 12
13	Model 13	Method 13	Results 13
14	Model 14	Method 14	Results 14
15	Model 15	Method 15	Results 15
16	Model 16	Method 16	Results 16
17	Model 17	Method 17	Results 17
18	Model 18	Method 18	Results 18
19	Model 19	Method 19	Results 19
20	Model 20	Method 20	Results 20
21	Model 21	Method 21	Results 21
22	Model 22	Method 22	Results 22
23	Model 23	Method 23	Results 23
24	Model 24	Method 24	Results 24
25	Model 25	Method 25	Results 25
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40	Model 40	Method 40	Results 40
41	Model 41	Method 41	Results 41
42	Model 42	Method 42	Results 42
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44	Model 44	Method 44	Results 44
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86	Model 86	Method 86	Results 86
87	Model 87	Method 87	Results 87
88	Model 88	Method 88	Results 88
89	Model 89	Method 89	Results 89
90	Model 90	Method 90	Results 90
91	Model 91	Method 91	

[illegible][illegible]
$$\begin{aligned} \mathbb{E}[\mathcal{L}_\lambda] &= \mathbb{E}[\mathcal{L}_\lambda(\mathbf{y})] \\ &= \mathbb{E}[\mathcal{L}_\lambda(\mathbf{y})] \\ &= \mathbb{E}[\mathcal{L}_\lambda(\mathbf{y})] \\ &= \mathbb{E}[\mathcal{L}_\lambda(\mathbf{y})] \end{aligned}$$

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

[illegible]

α	β	γ	δ	ϵ	ζ	η	θ	ι	κ	λ	μ	ν	ξ	\omicron	π	ρ	σ	τ	υ	ϕ	χ	ψ	ω
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24

$$Z^h = \{000, 011\} \quad \{1\} \quad \{U_{\text{S}} - 0\} H^{-1}(1) \{7k_0\} S^{-1} \}$$
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1 APPL. CATION NUMBER:
 2 FILING DATE:
 3 CLASSIFICATION:
 4 NAME: EATON, R. 5564-4119 B
 5 REGISTRATION NUMBER: 5564-4119 B
 6 REFERENCE/OTHER NUMBER:
 7 INFORMATION NUMBER: 5564-4119 B
 8 TELEPHONE: (617) 477-9400
 9 TELEFAX: (617) 477-9400
 10 INFORMATION FOR SEQ. 10 NO. 1
 11 SEQUENCE CHARACTERISTICS:
 12 LENGTH: 40 amino acids
 13 TYPE: amino acid
 14 MOLECULE TYPE: protein
 15 US-09-730-174a-3

16 Query Match: 100.0% Score: 59; ID: 1; Length: 40;
 17 Base Local Similarity: 100.0%; ID: 1; No. Matches: 0;
 18 Matches: 12; Conservation: 0; Gaps: 0;
 19 1 SVSSEIOLMNLG 12
 20 1 SVSSEIOLMNLG 12

21 RESULT 7
 22 US-09-730-174a-3
 23 September 7, Application US-09-730-174a-3
 24 Filing Date: 02-01-1999
 25 CLASSIFICATION:
 26 NAME: EATON, R. 5564-4119 B
 27 REGISTRATION NUMBER: 5564-4119 B
 28 REFERENCE/OTHER NUMBER:
 29 INFORMATION NUMBER: 5564-4119 B
 30 TELEPHONE: (617) 477-9400
 31 TELEFAX: (617) 477-9400
 32 INFORMATION FOR SEQ. 10 NO. 1
 33 SEQUENCE CHARACTERISTICS:
 34 LENGTH: 40 amino acids
 35 TYPE: amino acid
 36 MOLECULE TYPE: protein
 37 FEATURES:
 38 OTHER INFORMATION: (1) (2) (3) (4) (5) (6) (7) (8) (9) (10) (11) (12) (13) (14) (15) (16) (17) (18) (19) (20) (21) (22) (23) (24) (25) (26) (27) (28) (29) (30) (31) (32) (33) (34) (35) (36) (37) (38) (39) (40) (41) (42) (43) (44) (45) (46) (47) (48) (49) (50) (51) (52) (53) (54) (55) (56) (57) (58) (59) (60) (61) (62) (63) (64) (65) (66) (67) (68) (69) (70) (71) (72) (73) (74) (75) (76) (77) (78) (79) (80) (81) (82) (83) (84) (85) (86) (87) (88) (89) (90) (91) (92) (93) (94) (95) (96) (97) (98) (99) (100) (101) (102) (103) (104) (105) (106) (107) (108) (109) (110) (111) (112) (113) (114) (115) (116) (117) (118) (119) (120) (121) (122) (123) (124) (125) (126) (127) (128) (129) (130) (131) (132) (133) (134) (135) (136) (137) (138) (139) (140) (141) (142) (143) (144) (145) (146) (147) (148) (149) (150) (151) (152) (153) (154) (155) (156) (157) (158) (159) (160) (161) (162) (163) (164) (165) (166) (167) (168) (169) (170) (171) (172) (173) (174) (175) (176) (177) (178) (179) (180) (181) 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1  FILING DATE: 12 AUG 1994
2  APPLICANT: WHITLOCK, Gordon F
3  NAME: WHITLOCK, Gordon F
4  REGISTRATION NO: 613 247 590
5  OPERATING SYSTEM: IBM PC COMPATIBLE
6  TELEPHONE: (613) 247-5900
7  TELEFAX: (613) 247-5900
8  INFORMATION FOR SEQUENCE: 4
9  SEQUENCE CHARACTERISTICS:
10 LENGTH: 41 amino acids
11 TYPE: amino acid
12 SCRAMBLING: 1
13 PEPIDGY: linear
14 MISCLETYPE: 1
15 US-09-730-174a-3

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QUALITY MATCH: 100.0% Score: 59 DB 1: Length: 41
Best Local Similarity: 100.0% Filed No: 0.00016
Matches: 12 Conservative: 0 Mismatches: 0 Gaps: 0
1  SVSETOLMIN: 12
14 1 SVSETOLMIN: 12

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RESULT 11
US-09-730-174a-3
Sequence 1, Application US/09264552
Patent No. 5955440
GENERAL INFORMATION:
APPLICANT: WHITLOCK, Gordon F
APPLICANT: WHITFIELD, James F.
APPLICANT: SUREWICZ, Witold
APPLICANT: SURE, Wlad L.
APPLICANT: NUSSENBERG, Witold
TITLE OF INVENTION: PARALLEL TREATMENT OF OSTEOPOROSIS
TITLE OF INVENTION: PARALLEL TREATMENT OF OSTEOPOROSIS
NUMBER OF SEQUENCES: 4
SEQUENCE ADDRESS:
ADDRESS: KIRBY, Rados, 18% Lakot
STREET: 112 Kent Street, 18% 70,
CITY: Ottawa
COUNTRY: Canada
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
FILING DATE: 12/08/94
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 540
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 540
NAME: JAMES, No. 5955440
REGISTRATION NUMBER: 540
PREFERENCE/SEQUENCE NUMBER: 540
TITLE INFORMATION: CHIRALITY
TELEPHONE: (613) 247-5900
TELEFAX: (613) 247-0000
INFORMATION FOR SEQUENCE: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
PEPIDGY: linear
MISCLETYPE: 1
US-09-730-174a-3

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QUALITY MATCH: 100.0% Score: 59 DB 1: Length: 41
Best Local Similarity: 100.0% Filed No: 0.00016
Matches: 12 Conservative: 0 Mismatches: 0 Gaps: 0
1  SVSETOLMIN: 12
14 1 SVSETOLMIN: 12

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RESULT 12
US-09-730-174a-3
Sequence 1, Application US/09264552
Patent No. 5955440
GENERAL INFORMATION:
APPLICANT: WHITLOCK, Gordon F
APPLICANT: WHITFIELD, James F.
APPLICANT: SUREWICZ, Witold
APPLICANT: SURE, Wlad L.
APPLICANT: NUSSENBERG, Witold
TITLE OF INVENTION: PARALLEL TREATMENT OF OSTEOPOROSIS
TITLE OF INVENTION: PARALLEL TREATMENT OF OSTEOPOROSIS
NUMBER OF SEQUENCES: 4
SEQUENCE ADDRESS:
ADDRESS: KIRBY, Rados, 18% Lakot
STREET: 112 Kent Street, 18% 70,
CITY: Ottawa
COUNTRY: Canada
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
FILING DATE: 12/08/94
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 540
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 540
NAME: JAMES, No. 5955440
REGISTRATION NUMBER: 540
PREFERENCE/SEQUENCE NUMBER: 540
TITLE INFORMATION: CHIRALITY
TELEPHONE: (613) 247-5900
TELEFAX: (613) 247-0000
INFORMATION FOR SEQUENCE: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
PEPIDGY: linear
MISCLETYPE: 1
US-09-730-174a-3

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QUALITY MATCH: 100.0% Score: 59 DB 1: Length: 41
Best Local Similarity: 100.0% Filed No: 0.00016
Matches: 12 Conservative: 0 Mismatches: 0 Gaps: 0
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RESULT 13
US-09-730-174a-3
Sequence 1, Application US/09264552
Patent No. 5955440
GENERAL INFORMATION:
APPLICANT: Barbier, Jean Re
APPLICANT: Morley, Paul

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US-09-730-174a-3

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NAME: [REDACTED]
ALIAS: [REDACTED]
ADDRESS: [REDACTED]
CITY: [REDACTED]
STATE: [REDACTED]
ZIP: [REDACTED]
COUNTRY: [REDACTED]
TELEPHONE: [REDACTED]
FAX: [REDACTED]
E-MAIL: [REDACTED]
WEB: [REDACTED]
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PAGE: [REDACTED]
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REMARKS: [REDACTED]

NAME: [REDACTED]
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ADDRESS: [REDACTED]
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REMARKS: [REDACTED]



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Matches 10; Conservative 11; P1s matches 11; Indels 0; Gaps 0;

QV 1 AVSEIQLMINIG 12
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DE 56 AVSDVKLVHRIG 67

RESULT 6

QV 1 AVSEIQLMINIG 12

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DE 56 AVSDVKLVHRIG 67

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DE 56 AVSDVKLVHRIG 67

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Query Match 66.1% Score 49; DB 16; Length 144;

Best Local Similarity 50.0% P1: No. 4;

Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

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1111111111

DE 56 AVSDVKLVHRIG 67

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us-09-730-174a-4.open.rsp

Genome version 1.0
Copyright (c) 1993-2000 Compugen Ltd.

QM protein - protein search, us-09-730-174a-4

Run on: September 12, 2002, 14:02:20, Search file: 09-11-Pericula
(without alignment)
21,702 hits

Title: us-09-730-174a-4

Perfect score: 61

Sequence: 1 SVS01_PTHN12

Scoring table: BD080M2
Gapop 10, Gapext 0

Searched: 09-09-04 09:45:44 87,974 residues

Total number of hits are 4794 (shown parameters: 1522)

Minimum DB seq length: 1
Maximum DB seq length: 29960000

Post-processing: Minimum Match 0.4
Maximum Match 1.0
List the first 47 summaries

Database: SwissProt_40

Pred. No. is the score of the hit predicted by the program, and is greater than or equal to the score of the result being and is derived by analysis of the total score after filtering.

SUMMARIES

Result No	Score	Match	Length	DB	Description
1	61	100.0	115	P_HV_C/NEA	P_2212 canis familiaris
2	58	97.1	115	P_HV_S/VTH	P_2253 bos taurus
3	55	90.2	115	P_HV_H/MAN	P_0170 homo sapien
4	55	90.2	115	P_HV_C/1	P_0170 sus scrofa
5	55	90.2	115	P_HV_R/NEA	P_0170 macaca fusc
6	52	85.2	115	P_HV_C/1	P_0170 rattus norv
7	52	85.2	115	P_HV_C/1	P_0170 gallus gall
8	49	63.9	176	P_HV_C/1	P_0170 palthevete
9	49	63.9	176	P_HV_C/1	P_0170 canis fusc
10	48	62.3	438	P_HV_C/1	P_0170 mycoplasma
11	38	62.3	438	P_HV_C/1	P_0170 chlamydia
12	38	62.3	438	P_HV_C/1	P_0170 mycoplasma
13	38	62.3	438	P_HV_C/1	P_0170 mycoplasma
14	37	60.7	353	P_HV_C/1	P_0170 mycoplasma
15	37	60.7	353	P_HV_C/1	P_0170 mycoplasma
16	37	60.7	353	P_HV_C/1	P_0170 mycoplasma
17	36	59.6	586	P_HV_C/1	P_0170 mycoplasma
18	36	59.6	586	P_HV_C/1	P_0170 mycoplasma
19	35	57.4	438	P_HV_C/1	P_0170 mycoplasma
20	34	55.7	884	P_HV_C/1	P_0170 mycoplasma
21	34	55.7	884	P_HV_C/1	P_0170 mycoplasma
22	34	55.7	884	P_HV_C/1	P_0170 mycoplasma
23	34	55.7	884	P_HV_C/1	P_0170 mycoplasma
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ALIGNMENTS

RESULT 1

PTHY_C/NEA STANDARD: PTH 115 AA.

01 01-01-1996 (Rel. 34, Create)

02 01-01-1996 (Rel. 34, Last sequence update)

03 15-JUL-1998 (Rel. 36, Last annotation update)

04 Parathyroid hormone precursor (parathyrin) (PTH).

05 PTH.

06 Canis familiaris (Dog).

07 Pukaroyia; Molaxia; Chordata; Craniata; Vertebrata; Euteleostomi;

08 Mammalia; Eutheria; Carnivora; Canidae; Canis.

09 NCBI_TaxID=9615;

10 [1]

11 SEQUENCE FROM H.A.

12 HISSUE-Parathyroid;

13 MEDLINE 9546959; PubMed 7642104;

14 Rosol T.J., Steinmeyer C.L., McManis L.K., Greene A.,

15 Hewille J.W., Capen C.C.

16 "Sequences of the cDNAs encoding canine parathyroid hormone-related

17 protein and parathyroid hormone."

18 Gene 168:241-243(1995).

19 -P- FUNCTION. PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN

20 BONE AND PREVENTING THEIR URINAL EXCRETION.

21 SIMILARITY. BELONGS TO THE PARATHYROID HORMONE FAMILY.

22 This SWISS-PROT entry is complete. It is produced through a collaboration

23 between the Swiss Institute of Bioinformatics and the EMBL outstation

24 at the European Bioinformatics Institute. There are no restrictions on its

25 use by non-profit institutions as long as its content is in no way

26 modified and this statement is not removed. Usage by and for commercial

27 entities requires a license agreement (see <http://www.isdb.ch>

28 or send an email to license@isdb.ch).

29

30 HBBL 015662; AAA02584.1;

31 HBBP 01268; L2W6.

32 InterPro: IPR001415; Parathyroid.

33 InterPro: IPR001415; Parathyroid.

34 Pfam: PF01279; Parathyroid.

35 Pfam: PF01279; Parathyroid.

36 Pfam: PF01279; Parathyroid.

37 Pfam: PF01279; Parathyroid.

38 Pfam: PF01279; Parathyroid.

39 Pfam: PF01279; Parathyroid.

40 Pfam: PF01279; Parathyroid.

41 Pfam: PF01279; Parathyroid.

42 Pfam: PF01279; Parathyroid.

43 Pfam: PF01279; Parathyroid.

44 Pfam: PF01279; Parathyroid.

45 Pfam: PF01279; Parathyroid.

46 Pfam: PF01279; Parathyroid.

47 Pfam: PF01279; Parathyroid.

Query Match 100.0%; Score 61; DB 1; Length 115;

Best Local Similarity 100.0%; Seed Nucleotide 0; Model 0;

Matches 1; Database 1; Model 0; Score 0;

01 1 SVS01_PTHN12

02 12 SVS01_PTHN12



CC myeloma and epidermal cancers of the head neck and esophagus. The
 CC present sequence is a PTH peptide, with a Ser residue at position 1 and
 CC a Glu residue at position 19. The Ser residue improves transmembrane
 CC signal and via phosphorylation (Tyr 2), whereas the Glu residue reduces the
 CC signal and line 1 binding. PTH peptides with a Glu residue at
 CC position 19 have increased bone formation in rat and human patients and so may be
 CC used as a PTH receptor antagonist in the treatment of the above mentioned
 CC disorders and fractures related.

XX Sequence 28 AA:

Query Match: 100.0% Score 59; DB 21; Length 28;
 Best Local Similarity: 100.0% Score 59; DB 22; Length 28;
 Matches: 125 Conserved: 125; Gaps: 0; Identities: 125; Gaps: 0.

QY 1 SVSEIOLMHLNLS 12

IR 1 SVSEIOLMHLNLS 12

RESULT 14

AA081074

11 AA081074 standard; peptide; 28 AA;

XX AA081074;

XX 26-JUN-2001 (first entry)

XX Human parathyroid hormone analogues SEQ ID 4.

XX Parathyroid hormone (PTH) blood calcium level regulator; osteopathic;

XX vulvovaginal bone growth; bone healing; osteoporosis; fracture; human.

XX Homo sapiens.

XX Synthetic.

XX Key Location/Qualif: 13

XX Modified-site 22 /note= "Forms a beta lactam ring with Glu at position 26"

XX Modified-site 26 /note= "Forms a beta lactam ring with Lys at position 26"

XX Modified-site 28 /note= "Forms a beta lactam ring with Glu at position 22"

XX Modified-site 28 /note= "C-terminal amide"

XX W2001074-A2

XX 29 MAR 2001.

XX 21-SEP-2000; 2000W0-CA01094.

XX 22-SEP-1999; 99US-040683.

XX (CANADA) NAT RES COUNCIL CANADA.

XX Barber J, Morley P, Whithield J, Willick SE.

XX WPI; 2001 100381/23.

XX New human parathyroid hormone (PTH) analog useful for stimulating bone

XX growth for restoring bone, for prevention of bone healing, and for

XX treating osteoporosis and normal fractures.

XX Claim 16; Fig 4; 34pp; English.

XX Parathyroid hormone (PTH) is a major regulator of blood calcium levels.

XX this invention relates to PTH analogues, or their salts. Use of the

XX analogues results in osteoporosis and vulvovaginal activity. The PTH

XX analogues are useful for treating a warm-blooded animal for stimulating

XX bone growth, for restoring bone, and for the promotion of bone healing

XX during the treatment of osteoporosis and normal fractures. The present

XX sequence represents an analogue of human parathyroid hormone.

XX

QC Sequence 28 AA;

Query Match: 100.0% Score 59; DB 22; Length 28;

Best Local Similarity: 100.0% Score 59; DB 22; Length 28;

Matches: 125 Conserved: 125; Gaps: 0; Identities: 125; Gaps: 0;

QY 1 SVSEIOLMHLNLS 12

IR 1 SVSEIOLMHLNLS 12

RESULT 14

AA081078

11 AA081078 standard; peptide; 28 AA;

XX AA081078;

XX 26-JUN-2001 (first entry)

XX Human parathyroid hormone analogues SEQ ID 6.

XX Parathyroid hormone (PTH) blood calcium level regulator; osteopathic;

XX vulvovaginal bone growth; bone healing; osteoporosis; fracture; human.

XX Homo sapiens.

XX Synthetic.

XX Key Location/Qualif: 13

XX Modified-site 17 /note= "Forms a beta lactam ring with Glu at position 17"

XX Modified-site 22 /note= "Forms a beta lactam ring with Lys at position 13"

XX Modified-site 26 /note= "Forms a beta lactam ring with Lys at position 26"

XX Modified-site 28 /note= "Forms a beta lactam ring with Glu at position 22"

XX Modified-site 28 /note= "C-terminal amide"

XX W2001074-A2.

XX 29 MAR 2001.

XX 21-SEP-2000; 2000W0-CA01094.

XX 22-SEP-1999; 99US-040683.

XX (CANADA) NAT RES COUNCIL CANADA.

XX Barber J, Morley P, Whithield J, Willick SE.

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XX growth for restoring bone, for prevention of bone healing, and for

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XX Claim 16; Fig 4; 34pp; English.

XX Parathyroid hormone (PTH) is a major regulator of blood calcium levels.

XX this invention relates to PTH analogues, or their salts. Use of the

XX analogues results in osteoporosis and vulvovaginal activity. The PTH

XX analogues are useful for treating a warm-blooded animal for stimulating

XX bone growth, for restoring bone, and for the promotion of bone healing

XX during the treatment of osteoporosis and normal fractures. The present

XX sequence represents an analogue of human parathyroid hormone.

XX

QC Sequence 28 AA;

Query Match: 100.0% Score 59; DB 22; Length 28;

Best Local Similarity: 100.0% Score 59; DB 22; Length 28;

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us-09-730-174a-4.open.rpr

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ATTACHMENTS

us-09-730-174a-4.open.rpr

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REFERENCES

us-09-730-174a-4.open.rpr

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 51 42 AVSPELEPHNIN: 4
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Tuller	US-69-174A-1
Porter sequence	59
Sequence	1 SVSF, MINL 12
Synthetic data	PLSMB,
	CHARTER, CHARTER

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Total number of hits satisfying the search criteria: 1
Minimum: 0.000000
Maximum: 0.000000
Post processing: Minimum: 0.000000
Maximum: 0.000000
Processing time: 0.000000

Calculus : $\frac{1}{2} \sqrt{1-x^2} + \frac{1}{2} \ln \left| \frac{1}{1-x^2} \right| + C$

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3)	35	59.3	884	1	J-V-WB	DNA-directed DNA p
1	35	59.3	929	2	1.4532	hypothetical prote
2	35	59.3	1371	2	3.0241	sensory transducti
3	35	59.3	2570	2	1.4531	limbicae-associate
4	35	57.6	167	2	0.4460	hypothetical prote
5	35	57.6	167	2	3.1173	hypothetical prote
6	35	57.6	167	4	54.0957	hypothetical prote
7	35	57.6	256	2	1.45197	conserved hypothel
8	35	57.6	275	2	1.4530	hypothetical L-ser
9	35	57.6	309	2	4.2771	hypothetical prote
10	35	57.6	315	2	1.4539	conserved hypothel
11	35	57.6	365	2	4.0157	A/G-specific adenil
12	35	57.6	365	2	4.1145	A/G-specific adenil
13	35	57.6	374	2	4.1473	probable regulator
14	35	57.6	441	2	4.1225	amino-acid N-acety
15	35	57.6	443	1	X100AA	amino-acid N-acety

GENEID :
LOC :
Genetaphroid homotome precursor - pi:
Species: Sus scrofa domestica (domestic pig)
Date: 24 May 1974 #09-0685 (J) 111 Apr 1976 #10-1446 (J) 18-Jun-1999
Accession: K26806; A0147; A0145
Nucleotide sequence: Gross, G.; Wilson, G., Mayor, H.
Nucleic Acids Res. 15, 6740, 1987
Note: This is a revised sequence of a cDNA clone encoding preprogenitaphroid b
Reference number: K26806; M010873-938

ANAL. Calcd. for $C_{10}H_{12}O$: C, 85.69%; H, 8.81%. Found: C, 85.6%; H, 8.8%. IR (KBr): 3300 (broad), 1650 (strong), 1600 (strong), 1550 (strong), 1500 (strong), 1450 (strong), 1400 (strong), 1350 (strong), 1300 (strong), 1250 (strong), 1200 (strong), 1150 (strong), 1100 (strong), 1050 (strong), 1000 (strong), 950 (strong), 900 (strong), 850 (strong), 800 (strong), 750 (strong), 700 (strong), 650 (strong), 600 (strong), 550 (strong), 500 (strong), 450 (strong), 400 (strong), 350 (strong), 300 (strong), 250 (strong), 200 (strong), 150 (strong), 100 (strong). ¹H NMR (CDCl₃): δ 7.2 (d, 2H, J = 8.0 Hz), 6.8 (d, 2H, J = 8.0 Hz), 6.4 (d, 2H, J = 8.0 Hz), 6.0 (d, 2H, J = 8.0 Hz), 5.6 (d, 2H, J = 8.0 Hz), 5.2 (d, 2H, J = 8.0 Hz), 4.8 (d, 2H, J = 8.0 Hz), 4.4 (d, 2H, J = 8.0 Hz), 4.0 (d, 2H, J = 8.0 Hz), 3.6 (d, 2H, J = 8.0 Hz), 3.2 (d, 2H, J = 8.0 Hz), 2.8 (d, 2H, J = 8.0 Hz), 2.4 (d, 2H, J = 8.0 Hz), 2.0 (d, 2H, J = 8.0 Hz), 1.6 (d, 2H, J = 8.0 Hz), 1.2 (d, 2H, J = 8.0 Hz), 0.8 (d, 2H, J = 8.0 Hz). Mass (EI): m/z 152 (M⁺), 134 (M⁺ - 18), 116 (M⁺ - 36), 98 (M⁺ - 54), 80 (M⁺ - 72), 62 (M⁺ - 90), 44 (M⁺ - 108), 26 (M⁺ - 126). High-resolution mass spectrometry: m/z 152.0734 (M⁺), 134.0556 (M⁺ - 18), 116.0378 (M⁺ - 36), 98.0199 (M⁺ - 54), 80.0021 (M⁺ - 72), 62.0043 (M⁺ - 90), 44.0065 (M⁺ - 108), 26.0087 (M⁺ - 126). Literature values: IR (KBr): 3300 (broad), 1650 (strong), 1600 (strong), 1550 (strong), 1500 (strong), 1450 (strong), 1400 (strong), 1350 (strong), 1300 (strong), 1250 (strong), 1200 (strong), 1150 (strong), 1100 (strong), 1050 (strong), 1000 (strong), 950 (strong), 900 (strong), 850 (strong), 800 (strong), 750 (strong), 700 (strong), 650 (strong), 600 (strong), 550 (strong), 500 (strong), 450 (strong), 400 (strong), 350 (strong), 300 (strong), 250 (strong), 200 (strong), 150 (strong), 100 (strong). ¹H NMR (CDCl₃): δ 7.2 (d, 2H, J = 8.0 Hz), 6.8 (d, 2H, J = 8.0 Hz), 6.4 (d, 2H, J = 8.0 Hz), 6.0 (d, 2H, J = 8.0 Hz), 5.6 (d, 2H, J = 8.0 Hz), 5.2 (d, 2H, J = 8.0 Hz), 4.8 (d, 2H, J = 8.0 Hz), 4.4 (d, 2H, J = 8.0 Hz), 4.0 (d, 2H, J = 8.0 Hz), 3.6 (d, 2H, J = 8.0 Hz), 3.2 (d, 2H, J = 8.0 Hz), 2.8 (d, 2H, J = 8.0 Hz), 2.4 (d, 2H, J = 8.0 Hz), 2.0 (d, 2H, J = 8.0 Hz), 1.6 (d, 2H, J = 8.0 Hz), 1.2 (d, 2H, J = 8.0 Hz), 0.8 (d, 2H, J = 8.0 Hz). Mass (EI): m/z 152 (M⁺), 134 (M⁺ - 18), 116 (M⁺ - 36), 98 (M⁺ - 54), 80 (M⁺ - 72), 62 (M⁺ - 90), 44 (M⁺ - 108), 26 (M⁺ - 126). High-resolution mass spectrometry: m/z 152.0734 (M⁺), 134.0556 (M⁺ - 18), 116.0378 (M⁺ - 36), 98.0199 (M⁺ - 54), 80.0021 (M⁺ - 72), 62.0043 (M⁺ - 90), 44.0065 (M⁺ - 108), 26.0087 (M⁺ - 126).

[illegible]

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Midrib Leaf Consistent Use	0	0.000000000	0 days

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	1111111111
4	SVSE1QUMN13 43
	1111111111



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 3 INFORMATION FOR SEQ ID NO: 1
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 7 topology: linear
 8 MODEL TYPE: protein
 9 HYDROPHOBICITY: N
 10 FRAGMENT TYPE: N-terminal
 11 US-09-144,000-2

Query Match: 95.17% Identity: 100.00% DB 1: Large
 Best Local Similarity: 91.79% ID: 5717062
 Matches: 11; Conservative: 0; Gaps: 0;

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110 1 AVSELOPMNIG 12

RESULT 5

US-09-448,000-2
 Sequence: Application US/084841

Patent No. 5717062

GENERAL INFORMATION:

APPLICANT: Rosenblatt, Michael

INVENTOR: Rosenblatt, Michael

ADDRESS: Fish & Richardson P.C.

APPLICANT: Fish & Richardson P.C.

ADDRESS: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPIER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPIER: IBM PC compatible

OPERATING SYSTEM: PC DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 07/397,100

FILE DATE: 07-JUN-1995

CLASSIFICATION: 530

ACTING AGENT: INFORMATION:

NAME: Tracy, Y. Rocky

REGISTRATION NUMBER: 04,065

REFERENCE/BOOK NUMBER: 7/1 2001

OTHER INFORMATION: INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 1

SEQUENCE CHARACTERISTICS:

LENGTH: 415 amino acids

TYPE: amino acid

CLASSIFICATION: not relevant

TOPOLOGY: linear

MODEL TYPE: protein

FEATURE:

OTHER INFORMATION: The side chains of lys at

positions 17 and 18 are linked by an amide b

OTHER INFORMATION: and this sequence has an amide C-terminus (i.e., CONH2), r

OTHER INFORMATION: has a C-terminus (i.e., CONH2).

US-09-448,000-2

Query Match: 95.17% Identity: 100.00% DB 1: Large

Best Local Similarity: 91.79% ID: 5717062

Matches: 11; Conservative: 0; Gaps: 0;

107 1 VSSELOPMNIG 12

110 1 AVSELOPMNIG 12

RESULT 7

US-09-448,000-2
 Sequence: Application US/084841

Patent No. 5717062

GENERAL INFORMATION:

APPLICANT: Rosenblatt, Michael

INVENTOR: Rosenblatt, Michael

ADDRESS: Fish & Richardson P.C.

APPLICANT: Fish & Richardson P.C.

ADDRESS: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPIER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPIER: IBM PC compatible

OPERATING SYSTEM: PC DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 07/397,100

FILE DATE: 07-JUN-1995

CLASSIFICATION: 530

ACTING AGENT: INFORMATION:

NAME: Tracy, Y. Rocky

REGISTRATION NUMBER: 04,065

REFERENCE/BOOK NUMBER: 7/1 2001

OTHER INFORMATION: INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 1

SEQUENCE CHARACTERISTICS:

LENGTH: 415 amino acids

TYPE: amino acid

CLASSIFICATION: not relevant

TOPOLOGY: linear

MODEL TYPE: protein

FEATURE:

OTHER INFORMATION: The side chains of lys at

positions 17 and 18 are linked by an amide b

OTHER INFORMATION: and this sequence has an amide C-terminus (i.e., CONH2), r

OTHER INFORMATION: has a C-terminus (i.e., CONH2).

US-09-448,000-2

Query Match: 95.17% Identity: 100.00% DB 1: Large

Best Local Similarity: 91.79% ID: 5717062

Matches: 11; Conservative: 0; Gaps: 0;

107 1 VSSELOPMNIG 12

110 1 AVSELOPMNIG 12

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00 Treatment of the 120 wet weight solids. In addition, the present
XX sequence was added to the 120 wet weight solids.
SQ sequence 24 AA.

0017 1 AVSEIQLMHNLG 12
100.00; Score 59; DR 21; Length 28;
Best Local Similarity 100.00; E-Val. No. 0.00036;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0018 1 AVSEIQLMHNLG 12
100.00; Score 59; DR 21; Length 28;
Best Local Similarity 100.00; E-Val. No. 0.00036;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0019 1 AVSEIQLMHNLG 12
100.00; Score 59; DR 21; Length 28;
Best Local Similarity 100.00; E-Val. No. 0.00036;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0020 1 AVSEIQLMHNLG 12
100.00; Score 59; DR 21; Length 28;
Best Local Similarity 100.00; E-Val. No. 0.00036;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0021 1 AVSEIQLMHNLG 12
100.00; Score 59; DR 21; Length 28;
Best Local Similarity 100.00; E-Val. No. 0.00036;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0022 1 AVSEIQLMHNLG 12
100.00; Score 59; DR 21; Length 28;
Best Local Similarity 100.00; E-Val. No. 0.00036;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0023 1 AVSEIQLMHNLG 12
100.00; Score 59; DR 21; Length 28;
Best Local Similarity 100.00; E-Val. No. 0.00036;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0024 1 AVSEIQLMHNLG 12
100.00; Score 59; DR 21; Length 28;
Best Local Similarity 100.00; E-Val. No. 0.00036;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0017 1 AVSEIQLMHNLG 12
100.00; Score 59; DR 21; Length 28;
Best Local Similarity 100.00; E-Val. No. 0.00036;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0018 1 AVSEIQLMHNLG 12
100.00; Score 59; DR 21; Length 28;
Best Local Similarity 100.00; E-Val. No. 0.00036;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0019 1 AVSEIQLMHNLG 12
100.00; Score 59; DR 21; Length 28;
Best Local Similarity 100.00; E-Val. No. 0.00036;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0020 1 AVSEIQLMHNLG 12
100.00; Score 59; DR 21; Length 28;
Best Local Similarity 100.00; E-Val. No. 0.00036;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0021 1 AVSEIQLMHNLG 12
100.00; Score 59; DR 21; Length 28;
Best Local Similarity 100.00; E-Val. No. 0.00036;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0022 1 AVSEIQLMHNLG 12
100.00; Score 59; DR 21; Length 28;
Best Local Similarity 100.00; E-Val. No. 0.00036;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0023 1 AVSEIQLMHNLG 12
100.00; Score 59; DR 21; Length 28;
Best Local Similarity 100.00; E-Val. No. 0.00036;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0024 1 AVSEIQLMHNLG 12
100.00; Score 59; DR 21; Length 28;
Best Local Similarity 100.00; E-Val. No. 0.00036;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0025 1 AVSEIQLMHNLG 12
100.00; Score 59; DR 21; Length 28;
Best Local Similarity 100.00; E-Val. No. 0.00036;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Figure 1. The effect of the concentration of the *Agrobacterium* suspension on the transformation efficiency of *Agrobacterium* strains. The *Agrobacterium* strains were grown in YEA medium for 24 h at 28 °C. The cell concentration was adjusted to 10⁸ cells/ml. The cells were then mixed with the plant tissue and incubated for 24 h at 28 °C. The plant tissue was then cultured on the selective medium. The transformation efficiency was determined as the number of transformants per 100 µg of plant tissue. The data are the mean ± SD of three independent experiments.

— 2 —

Figure 1

Flowchart illustrating the selection process for the study.

The flowchart shows the progression from initial identification to final inclusion in the meta-analysis:

- Identification of studies through database searches and references.
- Screening based on title and abstract.
- Full-text screening.
- Inclusion in the meta-analysis.

The number of studies at each stage is indicated by the numbers in the boxes.

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Figure 1

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1. **Introduction**
 2. **Background**
 3. **Methodology**
 4. **Results**
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 217. **Figure 209**

[illegible]

Age Group	Men (%)	Women (%)
18-29	~65	~60
30-49	~55	~65
50-69	~65	~55
70+	~55	~65

[illegible]

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2002-09-22 09:46:08

DT 06-APR-1992 (first entry)
 DE Sequence of parathyroid hormone (1-34) analogue [Tyr34, bPTH(1-34)NH2].
 KW Parathyroid hormone analogues; osteoporosis therapy; hypercalcaemia;
 KW hyperparathyroidism; hormone dependent tumour; blood sugar; diabetes;
 KW insulin.
 XX
 XX Bos taurus.
 XX
 XX Key: 100% identity.
 DE Misconcl. reference 23.
 FT /total: phe, leu, met, val, tyr,
 FT histanyl, arg, ala, alpha-naphthyl, ala
 FT 3 30
 FT /total: "a s e c a a d"
 FT 4 30
 FT /total: "a s e c a a d"
 FT 5 30
 FT /total: "a s e c a a d"
 FT 7 30
 FT /total: "a s e c a a d"
 XX
 XX US4771124-A.
 XX
 XX 23-SEP-1988.
 XX
 XX 26-MAY-1997: 97% identity.
 XX
 XX 26-MAY-1997: 97% identity.
 XX
 XX (MSP) : MERCK & CO INC.
 XX
 XX Rosenblatt M, Caporale JJ, Neri R, Levy JD, Chores M,
 XX WPL 1988-274169/36.
 XX
 XX Parathyroid hormone peptide analogues - used for treatment
 XX osteoporosis, hypercalcaemia, hyperparathyroidism and tumour-
 XX dependent tumours, and in vitro bioassays.
 XX
 XX Claim 2: column 3; 6pp; English.
 XX
 XX The PTH analogues of the invention are used for inhibiting the
 XX naturally occurring hormone in vivo and in vitro, they have high
 XX binding affinity for their respective PTH receptors while not
 XX stimulating production of secondary messenger molecules, they may be used
 XX in vitro in a bioassay for PTH and a drug for the PTH analogues.
 XX They are prepared in dosage forms for oral, parenteral, topical, intra-
 XX nasal or topical use.
 XX
 XX Sequence: 34 AA:
 XX
 XX Query Match 100.0% Score 61; DB 9; Length 34;
 XX Best Local Similarity 100.0% Ident No. 0.00019;
 XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
 QY 1 AVSFQPMHNLG 12
 DE 1 avsfqpmhnlq 12
 XX
 XX RESULT: 6
 XX 27337521
 XX 00 AAR07921 standard; protein: 3; AA.
 XX
 XX AAR07921;
 XX
 XX 18-FEB-1991 (first entry)
 XX
 XX Bovine parathyroid hormone analogue, Tyr34 bPTH(7-34).
 XX
 XX Osteoporosis, hypercalcaemia, hyperparathyroidism, hypertension.
 XX
 XX Bos taurus.
 XX
 XX US4968669-A.
 XX
 XX 06-NOV-1990.
 XX
 XX 21-APR-1989: 890S-0341597.
 XX
 XX 21-APR-1989: 890S-0341597.
 XX
 XX 09-MAY-1988: 880S-0191512.
 XX
 XX (MERT) MERCK & CO INC.
 XX
 XX Rosenblatt M, Chores M;
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 XX 21-APR-1989: 890S-0341597.
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 XX 21-APR-1989: 890S-0341597.
 XX
 XX 09-MAY-1988: 880S-0191512.
 XX
 XX (MERT) MERCK & CO INC.
 XX
 XX Rosenblatt M, Chores M;
 XX

XX Osteoporosis; hypercalcaemia; hyperparathyroidism; hypertension.
 XX
 XX Bos taurus.
 XX
 XX US4968669-A.
 XX
 XX 06-NOV-1990.
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 XX 21-APR-1989: 890S-0341597.
 XX
 XX 21-APR-1989: 890S-0341597.
 XX
 XX 09-MAY-1988: 880S-0191512.
 XX
 XX (MERT) MERCK & CO INC.
 XX
 XX Rosenblatt M, Chores M;
 XX
 XX WPL 1990 354542/47.
 XX
 XX New parathyroid hormone analogues which inhibit hormone
 XX activity by binding receptors while not producing second
 XX messenger molecules
 XX
 XX Claim 1: Column 8; 6pp; English.
 XX
 XX Peptide analogues have high affinity for PTH cell surface receptors,
 XX but do not stimulate production of secondary messenger molecules.
 XX They may be used in inhibition of PTH action, and in diagnosis and
 XX treatment of osteoporosis, hypercalcaemia and hyperparathyroidism.
 XX Analogues may also be used in treatment of tumours and other cells
 XX overproducing peptide hormone like substances, and immune diseases
 XX such as allergic inflammation and hyperactive lymphocytes.
 XX Naturally occurring PTH levels may also be measured in vitro.
 XX
 XX Sequence: 34 AA:
 XX
 XX Query Match 100.0% Score 61; DB 11; Length 34;
 XX Best Local Similarity 100.0% Ident No. 0.00019;
 XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
 QY 1 AVSFQPMHNLG 12
 DE 1 avsfqpmhnlq 12
 XX
 XX RESULT: 6
 XX 27337521
 XX 00 AAR07921 standard; protein: 3; AA.
 XX
 XX AAR07921;
 XX
 XX 18-FEB-1991 (first entry)
 XX
 XX Bovine parathyroid hormone analogue, Tyr34 bPTH(7-34).
 XX
 XX Osteoporosis, hypercalcaemia, hyperparathyroidism, hypertension.
 XX
 XX Bos taurus.
 XX
 XX US4968669-A.
 XX
 XX 06-NOV-1990.
 XX
 XX 21-APR-1989: 890S-0341597.
 XX
 XX 21-APR-1989: 890S-0341597.
 XX
 XX 09-MAY-1988: 880S-0191512.
 XX
 XX (MERT) MERCK & CO INC.
 XX
 XX Rosenblatt M, Chores M;
 XX

SQ Sequence 1: AA

Query Match 100.0%; Score 61; DB 14; Length 41;
 Best Local Similarity 100.0%; Pos. No. 0.00019;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQFMHNG 1;
 1111111111;
 Db 1 avseiqfmhng 1;

RESULT 14

AAR34344
 ID AAR34344 standard; peptide; 34 AA;

XX AC
 AC AAR34344;

DE 04-APR-1993 (first entry)

XX DE Bovine parathyroid hormone analogue.

XX DE bPTH mutant, substitution, osteoporosis, bone disease, calcium;

KW hypertension; smooth muscle relaxation; cardiac inotropism;

KW chromotropy; side effects; analogue.

XX OS Synthetic.

XX KEY Location/Qual: ers

FT Misc-difference 24

FI /notes "W236 mutation"

XX W09306846-A.

XX 15-APR-1993.

XX 09-OCT-1992; 92WG-US08478.

XX 10-OCT-1992; 91US-0773097.

XX (PAM?) FANG P K T.

XX Pang PKT, Shan J;

XX WPT: 1993-134128/16.

XX Analogues of human and bovine parathyroid hormone with

PI substitution at amino acid 23 for treating osteoporosis without

XX side effects on heart or smooth muscle

XX Claim 9; Fig 2b; 116pp; English

CC The sequence shows a bovine parathyroid hormone analog comprising
 CC a substit. at amino acid residue 23 (Trp in wild type sequence). The
 CC analogues are useful for treating osteoporosis and other bone diseases
 CC involving calcium regulation. Unlike the natural hormone, the synthetic
 CC analogues do not cause hypertension, smooth muscle relaxation or cardiac
 CC inotropic or chronotropic side effects.

CC See also AAR34335-70.

XX Sequence 34 AA

Query Match 100.0%; Score 61; DB 14; Length 41;
 Best Local Similarity 100.0%; Pos. No. 0.00019;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQFMHNG 1;
 1111111111;
 Db 1 avseiqfmhng 1;

RESULT 15

AAR34345

ID AAR34345 standard; peptide; 34 AA;

XX AC

XX AAR34345;

DE 04-APR-1993 (first entry)

XX DE Bovine parathyroid hormone analogue.

XX DE bPTH mutant, substitution, osteoporosis, bone disease, calcium;

KW hypertension; smooth muscle relaxation; cardiac inotropism;

KW chromotropy; side effects; analogue.

XX OS Synthetic.

XX KEY Location/Qual: ers

FT Misc-difference 24

FI /notes "W236 mutation"

XX W09306846-A.

XX 15-APR-1993.

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XX Pang PKT, Shan J;

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XX Claim 9; Fig 21; 116pp; English

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CC analogues do not cause hypertension, smooth muscle relaxation or cardiac

CC inotropic or chronotropic side effects.

CC See also AAR34335-70.

XX Sequence 34 AA;

Query Match 100.0%; Score 61; DB 14; Length 34;

Best Local Similarity 100.0%; Pos. No. 0.00019;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQFMHNG 12

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QY 9 HENEG 12
DE 1 1
DE 4 YNFG 7

RESULT 14
ID IP02_MOUSE
AC P48640

DI 01-OCT-1994 (Rel. 39, Created)
DI 01-OCT-1994 (Rel. 39, Last sequence update)
DI 01-FEB-1995 (Rel. 40, Last annotation update)

DE 01-FEB-1995 (Rel. 40, Last annotation update)
DE 01-FEB-1995 (Rel. 40, Last annotation update)
DE 01-FEB-1995 (Rel. 40, Last annotation update)

OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Muridae
OX NCBI_TaxID:10090

RN 111
RT TISSUE: Fibroblast
RC TISSUE: Skin
RX MIM: 155490, P. Med. 922101

RA MIM: 155490, P. Med. 922101
RA MIM: 155490, P. Med. 922101
RA MIM: 155490, P. Med. 922101

RI "Separation and sequencing of human and novel murine proteins
RI "Separation and sequencing of human and novel murine proteins
RI "Separation and sequencing of human and novel murine proteins"

RI "Electrophoresis of 5-74 kDa (p48640)
RI "Electrophoresis of 5-74 kDa (p48640)
RI "Electrophoresis of 5-74 kDa (p48640)"

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Muridae
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Muridae
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Muridae

OX NCBI_TaxID:10090
OX NCBI_TaxID:10090
OX NCBI_TaxID:10090

RN 111
RT TISSUE: Fibroblast
RC TISSUE: Skin
RX MIM: 155490, P. Med. 922101

RA MIM: 155490, P. Med. 922101
RA MIM: 155490, P. Med. 922101
RA MIM: 155490, P. Med. 922101

RI "Separation and identification of multiple neuropeptides in the
RI "Separation and identification of multiple neuropeptides in the
RI "Separation and identification of multiple neuropeptides in the"

RI "Isolation and identification of multiple neuropeptides in the
RI "Isolation and identification of multiple neuropeptides in the
RI "Isolation and identification of multiple neuropeptides in the"

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Muridae
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Muridae
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Muridae

OX NCBI_TaxID:10090
OX NCBI_TaxID:10090
OX NCBI_TaxID:10090

QY 9 HENEG 12
DE 1 1
DE 4 YNFG 9

RESULT 15
ID IP02_MOUSE
AC P48640

DI 01-OCT-1994 (Rel. 39, Created)
DI 01-OCT-1994 (Rel. 39, Last sequence update)
DI 01-FEB-1995 (Rel. 40, Last annotation update)

DE 01-FEB-1995 (Rel. 40, Last annotation update)
DE 01-FEB-1995 (Rel. 40, Last annotation update)
DE 01-FEB-1995 (Rel. 40, Last annotation update)

OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Muridae
OX NCBI_TaxID:10090

RN 111
RT TISSUE: Fibroblast
RC TISSUE: Skin
RX MIM: 155490, P. Med. 922101

RA MIM: 155490, P. Med. 922101
RA MIM: 155490, P. Med. 922101
RA MIM: 155490, P. Med. 922101

RI "Separation and sequencing of human and novel murine proteins
RI "Separation and sequencing of human and novel murine proteins
RI "Separation and sequencing of human and novel murine proteins"

RI "Electrophoresis of 5-74 kDa (p48640)
RI "Electrophoresis of 5-74 kDa (p48640)
RI "Electrophoresis of 5-74 kDa (p48640)"

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Muridae
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Muridae
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Muridae

OX NCBI_TaxID:10090
OX NCBI_TaxID:10090
OX NCBI_TaxID:10090

RN 111
RT TISSUE: Fibroblast
RC TISSUE: Skin
RX MIM: 155490, P. Med. 922101

RA MIM: 155490, P. Med. 922101
RA MIM: 155490, P. Med. 922101
RA MIM: 155490, P. Med. 922101

RI "Separation and identification of multiple neuropeptides in the
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OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Muridae
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Muridae
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Muridae

OX NCBI_TaxID:10090
OX NCBI_TaxID:10090
OX NCBI_TaxID:10090

Query Match 23.7% Score 14; DR 1; Length 10;
Best Local Similarity 40.0% Pos 4; 4.5e-03;
Matches 3; Conservative 1; Mismatches 1; Totals 0; Gaps 0;

QY 4 E Q 6
DE 1 1
DE 4 E Q 6

RESULT 14
ID ALL9_CARMA
AC P81822

DI 30-MAY-2000 (Rel. 39, Created)
DI 30-MAY-2000 (Rel. 39, Last sequence update)
DI 30-MAY-2000 (Rel. 39, Last sequence update)

DE 30-MAY-2000 (Rel. 39, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last sequence update)

OS Carcinus maenas (Green crab)
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca

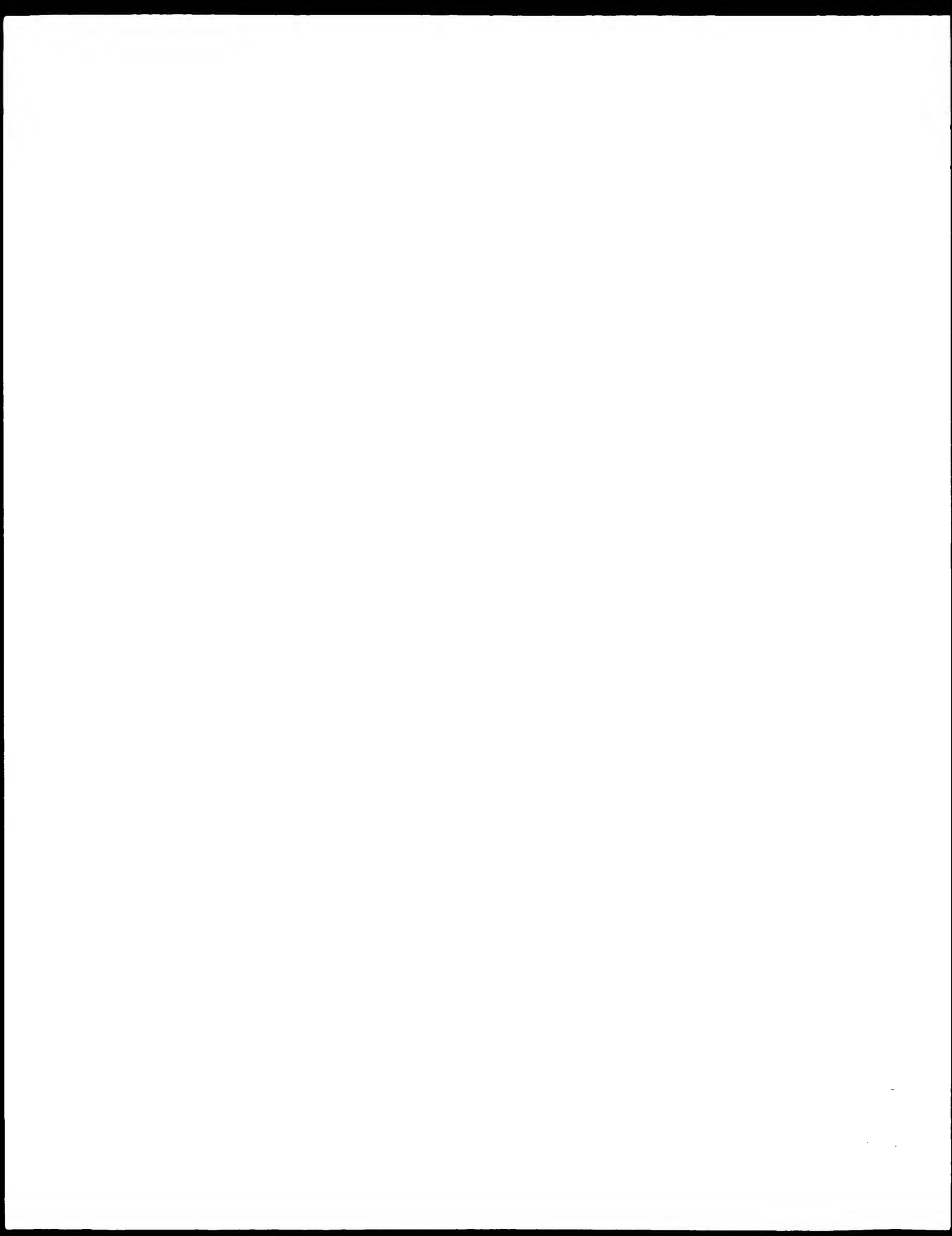
OX NCBI_TaxID:6759
OX NCBI_TaxID:6759
OX NCBI_TaxID:6759

RN 111
RT TISSUE: Cerebral ganglion and thoracic ganglion
RC TISSUE: Cerebral ganglion and thoracic ganglion
RX MIM: 642119, P. Med. 441250

RA MIM: 642119, P. Med. 441250
RA MIM: 642119, P. Med. 441250
RA MIM: 642119, P. Med. 441250

RI "Isolation and identification of multiple neuropeptides in the
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Chapter 10: Database Management

SQL: Structured Query Language

Run: C:\Program Files\Microsoft SQL Server\Binn\sqlservr.exe -s C:\Program Files\Microsoft SQL Server\Binn\sqlservr.exe -i C:\Program Files\Microsoft SQL Server\Binn\sqlservr.exe -m C:\Program Files\Microsoft SQL Server\Binn\sqlservr.exe -p C:\Program Files\Microsoft SQL Server\Binn\sqlservr.exe -u C:\Program Files\Microsoft SQL Server\Binn\sqlservr.exe -w C:\Program Files\Microsoft SQL Server\Binn\sqlservr.exe

File: C:\Program Files\Microsoft SQL Server\Binn\sqlservr.exe

Server: MSSQLSERVER

Database: MSSQLSERVER

Table: MSSQLSERVER.dbo.sysobjects

Field: MSSQLSERVER.dbo.sysobjects.name

Value: MSSQLSERVER.dbo.sysobjects.name

Length: MSSQLSERVER.dbo.sysobjects.name

Null: MSSQLSERVER.dbo.sysobjects.name

Index: MSSQLSERVER.dbo.sysobjects.name

PK: MSSQLSERVER.dbo.sysobjects.name

FK: MSSQLSERVER.dbo.sysobjects.name

Ref: MSSQLSERVER.dbo.sysobjects.name

Card: MSSQLSERVER.dbo.sysobjects.name

Order: MSSQLSERVER.dbo.sysobjects.name

Group: MSSQLSERVER.dbo.sysobjects.name

Usage: MSSQLSERVER.dbo.sysobjects.name

Comment: MSSQLSERVER.dbo.sysobjects.name

Default: MSSQLSERVER.dbo.sysobjects.name

Check: MSSQLSERVER.dbo.sysobjects.name

Trigger: MSSQLSERVER.dbo.sysobjects.name

View: MSSQLSERVER.dbo.sysobjects.name

Procedure: MSSQLSERVER.dbo.sysobjects.name

Function: MSSQLSERVER.dbo.sysobjects.name

Aggregate: MSSQLSERVER.dbo.sysobjects.name

Index: MSSQLSERVER.dbo.sysobjects.name

Constraint: MSSQLSERVER.dbo.sysobjects.name

Table: MSSQLSERVER.dbo.sysobjects.name

Field: MSSQLSERVER.dbo.sysobjects.name

Value: MSSQLSERVER.dbo.sysobjects.name

Length: MSSQLSERVER.dbo.sysobjects.name

Null: MSSQLSERVER.dbo.sysobjects.name

Index: MSSQLSERVER.dbo.sysobjects.name

PK: MSSQLSERVER.dbo.sysobjects.name

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Group: MSSQLSERVER.dbo.sysobjects.name

Usage: MSSQLSERVER.dbo.sysobjects.name

Comment: MSSQLSERVER.dbo.sysobjects.name

Default: MSSQLSERVER.dbo.sysobjects.name

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View: MSSQLSERVER.dbo.sysobjects.name

Procedure: MSSQLSERVER.dbo.sysobjects.name

Function: MSSQLSERVER.dbo.sysobjects.name

Aggregate: MSSQLSERVER.dbo.sysobjects.name

Index: MSSQLSERVER.dbo.sysobjects.name

Constraint: MSSQLSERVER.dbo.sysobjects.name

Table: MSSQLSERVER.dbo.sysobjects.name

Field: MSSQLSERVER.dbo.sysobjects.name

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Index: MSSQLSERVER.dbo.sysobjects.name

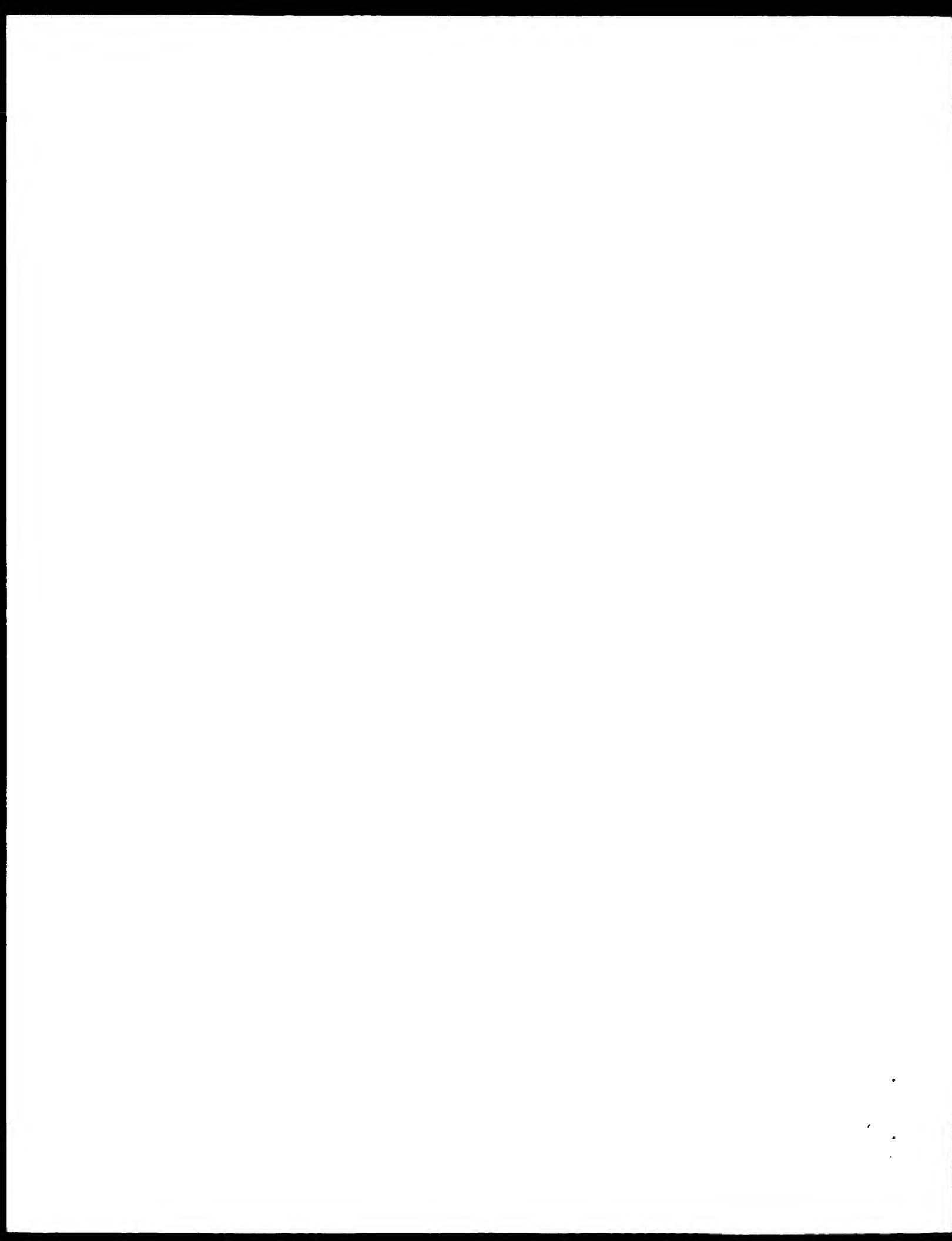
PK: MSSQLSERVER.dbo.sysobjects.name

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Sequence: 61

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us-09-730-174a-4 2.544 Mbits 6.01 updates/sec
 (without alignment)
 2.544 Mbits 6.01 updates/sec

ALIGNMENTS

us-09-730-174a-4 2.544 Mbits 6.01 updates/sec
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us-09-730-174a-4.closed.rsp



us-09-730-174a-4.closed.rag

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Search results for us-09-730-174a-4 (without alignment)

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14,923 hits found

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ALIGNMENTS

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Search results for us-09-730-174a-4 (without alignment)

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1  ZIP: 30303-416
2  MEDIUM READER: IBM
3  MEDIUM TYPE: floppy disk
4  COMPUTER: IBM PC compat
5  OPERATING SYSTEM: PC DOS/MS-DOS
6  SOFTWARE: Patent Release #1.0 Version #1.25
7  CURRENT APPLICATION DATA:
8  APPLICATION NUMBER: US/09/730-174
9  FILING DATE: 29 SEPT 1994
10 CLASSIFICATION:
11 A1P-PRI/A-ENT: 11
12 NAME: FROST, ROGER T.
13 REG STRALIN NUMBER: 11254
14 REFERENCE/DOCX NUMBER: 11254
15 TELECOMMUNICATION INFORMATION:
16 TELEPHONE: (404) 473-6794
17 TELEFAX: (404) 473-6794
18 INFORMATION FOR SEQ ID NO: 1
19 SEQUENCE CHARACTERISTICS:
20 LENGTH: 5 amino acids
21 TYPE: amino acid
22 PRT: YES
23 MEDIUM TYPE: floppy disk
24 HYDROPHILIC: N
25 US: 09-730-174a-4

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Best Local Similarity: 60.0%, ID: 1, No: 1.7e+05
Matches: 3, Conservative: 0, Mismatches: 0, Gaps: 0

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Q7 8 MINIG 12

16 1 LHM 5

RESULT 11

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1  US: 09-730-174a-4
2  Sequence: 39.9%, Seq: 24, ID: 24, Length: 5
3  Patent No: 5928892
4  GENERAL INFORMATION:
5  APPLICATION: Patent Release #1.0 Version #1.25
6  TITLE OF INVENTION: Method and device for detecting
7  NUMBER OF SEQUENCES: 36
8  CORRESPONDENCE ADDRESS:
9  ADDRESSEE: Jones & Askew, Inc.
10 STREET: 191 Peachtree Street, 3rd Floor
11 CITY: Atlanta
12 STATE: Georgia
13 COUNTRY: USA
14 ZIP: 30303
15 MEDIUM TYPE: floppy disk
16 COMPUTER: IBM PC compat
17 OPERATING SYSTEM: PC DOS/MS-DOS
18 SOFTWARE: Patent Release #1.0 Version #1.25
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: US/09/730-174
21 FILING DATE: 29 SEPT 1994
22 CLASSIFICATION:
23 A1P-PRI/A-ENT: 11
24 NAME: FROST, ROGER T.
25 REGISTRATION NUMBER: 11254
26 REFERENCE/DOCX NUMBER: 11254
27 INFORMATION FOR SEQ ID NO: 1
28 SEQUENCE CHARACTERISTICS:
29 LENGTH: 5 amino acids
30 TYPE: amino acid
31 PRT: YES
32 MEDIUM TYPE: floppy disk
33 HYDROPHILIC: N
34 US: 09-730-174a-4

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1  SEQUENCE CHARACTERISTICS:
2  LENGTH: 5 amino acids
3  TYPE: amino acid
4  PRT: YES
5  MEDIUM TYPE: floppy disk
6  HYDROPHILIC: N
7  US: 09-730-174a-4

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Query Match: 39.9%, Seq: 24, ID: 24, Length: 5
Best Local Similarity: 60.0%, ID: 1, No: 1.7e+05
Matches: 3, Conservative: 0, Mismatches: 0, Gaps: 0

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Q7 8 MINIG 12

16 1 LHM 5

RESULT 12

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1  US: 09-730-174a-4
2  Sequence: 39.9%, Seq: 24, ID: 24, Length: 5
3  Patent No: 6040790
4  GENERAL INFORMATION:
5  APPLICATION: Patent Release #1.0 Version #1.25
6  TITLE OF INVENTION: Peptides from the hPTH Sequence
7  NUMBER OF SEQUENCES: 36
8  CORRESPONDENCE ADDRESS:
9  ADDRESSEE: Jones & Askew, Inc.
10 STREET: 191 Peachtree Street, 3rd Floor
11 CITY: Atlanta
12 STATE: Georgia
13 COUNTRY: USA
14 ZIP: 30303
15 MEDIUM TYPE: floppy disk
16 COMPUTER: IBM PC compat
17 OPERATING SYSTEM: PC DOS/MS-DOS
18 SOFTWARE: Patent Release #1.0 Version #1.25
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: US/09/730-174
21 FILING DATE: 29 SEPT 1994
22 CLASSIFICATION:
23 A1P-PRI/A-ENT: 11
24 NAME: FROST, ROGER T.
25 REGISTRATION NUMBER: 11254
26 REFERENCE/DOCX NUMBER: 11254
27 INFORMATION FOR SEQ ID NO: 1
28 SEQUENCE CHARACTERISTICS:
29 LENGTH: 5 amino acids
30 TYPE: amino acid
31 PRT: YES
32 MEDIUM TYPE: floppy disk
33 HYDROPHILIC: N
34 US: 09-730-174a-4

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```

Query Match: 39.9%, Seq: 24, ID: 24, Length: 5
Best Local Similarity: 100.0%, ID: 1, No: 1.7e+05
Matches: 4, Conservative: 0, Mismatches: 0, Gaps: 0

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Q7 9 MINIG 12

11 1 LHM 4


```

: INFORMATION FOR SEQ 1: NO: 61
: SEQUENCE CHARACTERISTICS:
:   LENGTH: 8 amino acids
:   TYPE: amino acid
:   STRANDEDNESS: single
:   TOPOLOGY: linear
: FEATURE:
:   NAME/KEY: Modified site
:   LOCATION: 1
:   OTHER INFORMATION: Z: 4.00, "OTHER"
:   OTHER INFORMATION: /label: His
:   OTHER INFORMATION: /note: "acetylation"
US-08-748-021-64

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Query Match: 59.4% Score: 24; DB: 2; Length: 8;
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Matches: 4; Conservative: 0; Mismatches: 0; Gaps: 0;

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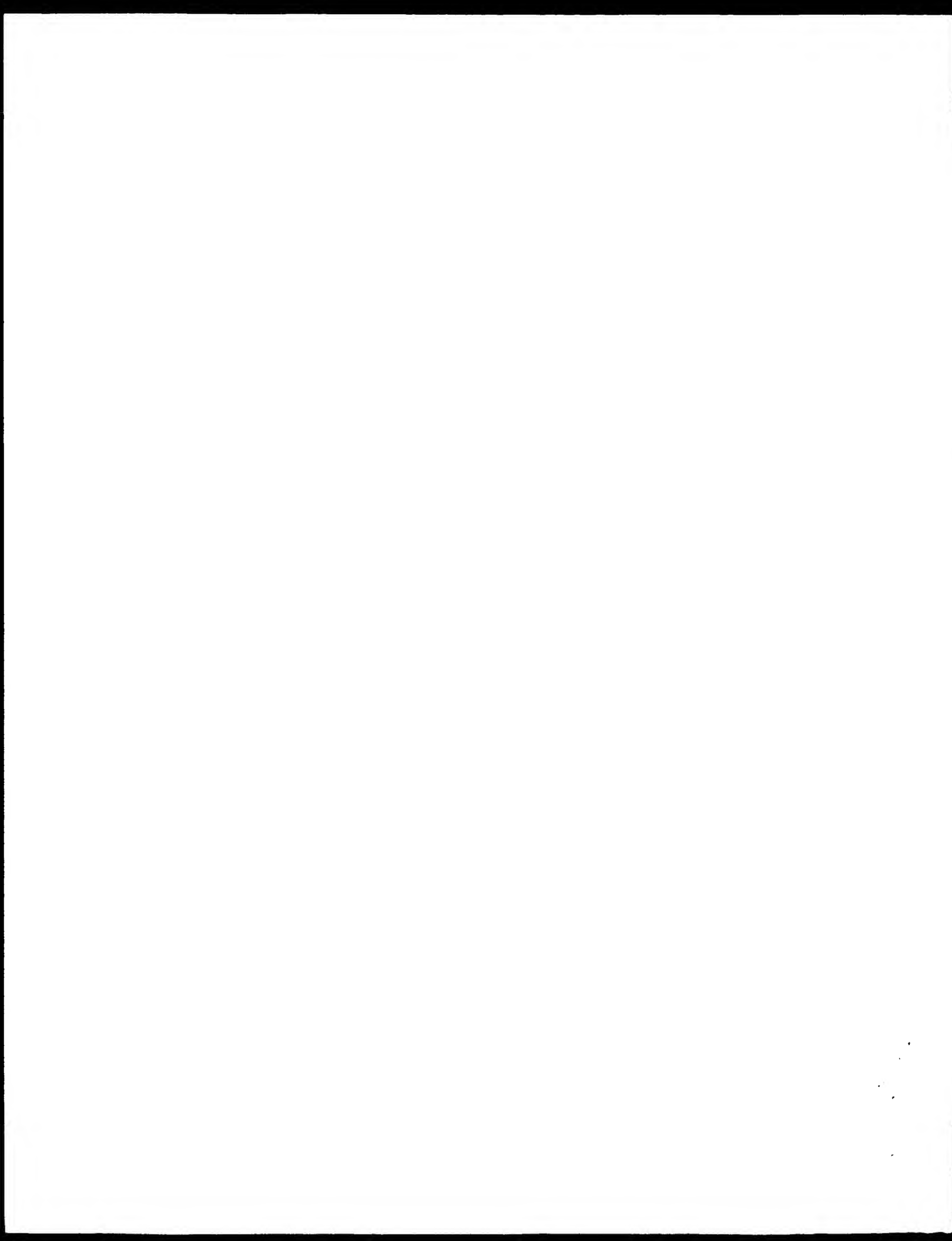
CY 5 HNG 12
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  2 HNG 5

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Search completed: September 21, 2002, 13:04:34
Job time: 131 sec

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Genome version 4.5
Copyright (c) 2002 Compugen Ltd.

PM protein - protein search using BLAST

Run on: Sept 19 21:20:16 07-16 Search time 11:57 seconds
(without alignments)
2,396,811 hits, 511,142,475 bytes

Title: US-09-730-174a-5

Perfect score: 59

Sequence: 1 AVAL1_MOUSE [2]

Scoring table: 400S 200

Gapop 1.00, expect 1.0

Searched: 2831000 seqs, 96000000 residues

Total number of hits satisfying chosen parameters: 1376

Minimum DB seq length: 9

Maximum DB seq length: 1

Post processing: Minimum Match 2

Maximum Match 100

Listing first 45 summaries

Database: 1: PIR711*

2: PIR2*

3: PIR3*

4: PIR4*

Pred. No. is the number of results predicted by choice to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

EMAP100

Result No.	Score	Match	Length	Description
1	21	65.6	12	1: heavy chain V r
2	18	60.5	9	2: A58718
3	18	60.5	9	3: A58718
4	18	60.5	10	4: A58718
5	18	60.5	10	5: A58718
6	18	60.5	12	6: A58718
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23	14	53.7	4	23: A58718
24	14	53.7	9	24: A58718
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29	14	53.7	11	29: A58718

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retinal oxidase -
acidic proline-rich
hypothetical prote
transcription fact
t-complex polypept
glutamine tRNA 11
p18 protein - Sal
cell receptor al
antitoxin-conver
hypothetical prote
leukokinin VI - Ma
14 heavy chain V-D-J r
coat protein beta
spontaneously p
14 heavy chain CDR

ALIGNMENTS

RESULT 1

S21205

14 heavy chain V region - human

C:Species: Homo sapiens (man)

C:Accession: S21205

R:Makiya, R.; Stigbrand, T.

Eur. J. Biochem. 205, 341-345, 1992

A:Title: Placental alkaline phosphatase has a binding site for the human immunoglobul

A:Accession: S21205

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-12 (MAK)

C:Keywords: heterodimer; immunoglobulin

Query Match: 25.6%; S21205; DB 2; Length 12;

Best Local Similarity: 44.4%; S21205; DB 2; Length 12;

Matches: 4; Conservative: 0; Mismatches: 2; Indels: 0; Gaps: 0;

Q: 4 EVOLVING 12

11 1 EVOLVING 9

RESULT 2

A58718

Carnocin 0149 - Carnobacterium sp. (fragment)

C:Species: Carnobacterium sp.

C:Accession: A58718

R:Stallard, G.; Nissen Meyer, J.; Jarmarsdottir, A.; Stetten, K.; Holo, H.; Nes, I.F.

Appl. Environ. Microbiol. 59, 1417-1422, 1993

A:Title: Purification and characterization of a new bacteriocin isolated from a Carno

A:Accession: A58718

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-7 (SIO)

C:Keywords: antibiotic; lanthionine

Query Match: 30.6%; SIO 6; DB 2; Length 7;

Best Local Similarity: 100.0%; SIO 6; DB 2; Length 7;

Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

Q: 3 SIO 6

11 1 SIO 5

Accession: 112000000

Query Match 28.9% (28.9% 17; DB 2; Length 12)

Best Local Similarity 44.1% (44.1% 17; DB 2; Length 12)

Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 112000000 1;

DB 1 112000000 9

RESULT 9

1 cell receptor alpha chain V region (V-9/10/1) human (fragment)

Species: Homo sapiens (human)

Accession: AF040946

Query Match 28.9% (28.9% 17; DB 2; Length 12)

Best Local Similarity 44.1% (44.1% 17; DB 2; Length 12)

Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 112000000 1;

DB 1 112000000 9

RESULT 10

1 cell receptor alpha chain V region (V-9/10/1) human (fragment)

Species: Homo sapiens (human)

Accession: AF040946

Query Match 28.9% (28.9% 17; DB 2; Length 12)

Best Local Similarity 44.1% (44.1% 17; DB 2; Length 12)

Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 112000000 1;

DB 1 112000000 9

RESULT 11

1 cell receptor alpha chain V region (V-9/10/1) human (fragment)

Species: Homo sapiens (human)

Accession: AF040946

Query Match 28.9% (28.9% 17; DB 2; Length 12)

Best Local Similarity 44.1% (44.1% 17; DB 2; Length 12)

Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 112000000 1;

DB 1 112000000 9

RESULT 12

1 cell receptor alpha chain V region (V-9/10/1) human (fragment)

Species: Homo sapiens (human)

Accession: AF040946

Query Match 28.9% (28.9% 17; DB 2; Length 12)

Best Local Similarity 44.1% (44.1% 17; DB 2; Length 12)

Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 112000000 1;

DB 1 112000000 9

RESULT 13

1 cell receptor alpha chain V region (V-9/10/1) human (fragment)

Species: Homo sapiens (human)

Accession: AF040946

Query Match 28.9% (28.9% 17; DB 2; Length 12)

Best Local Similarity 44.1% (44.1% 17; DB 2; Length 12)

Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 112000000 1;

DB 1 112000000 9

Accession: preliminary
Accession type: mRNA
Accession: 112000000Query Match 28.9% (28.9% 17; DB 2; Length 12)
Best Local Similarity 44.1% (44.1% 17; DB 2; Length 12)
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AVSR 4

DB 2 AVSR 5

RESULT 12

1 cell receptor alpha chain V region (V-9/10/1) human (fragment)

Species: Mus musculus (mouse)

Accession: AF040946

Query Match 28.9% (28.9% 17; DB 2; Length 12)

Best Local Similarity 44.1% (44.1% 17; DB 2; Length 12)

Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AVSR 4

DB 2 AVSR 5

RESULT 13

1 cell receptor alpha chain V region (V-9/10/1) human (fragment)

Species: Mus musculus (mouse)

Accession: AF040946

Query Match 28.9% (28.9% 17; DB 2; Length 12)

Best Local Similarity 44.1% (44.1% 17; DB 2; Length 12)

Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AVSR 4

DB 2 AVSR 5

RESULT 14

1 cell receptor alpha chain V region (V-9/10/1) human (fragment)

Species: Mus musculus (mouse)

Accession: AF040946

Query Match 28.9% (28.9% 17; DB 2; Length 12)

Best Local Similarity 44.1% (44.1% 17; DB 2; Length 12)

Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AVSR 4

DB 2 AVSR 5

RESULT 15

1 cell receptor alpha chain V region (V-9/10/1) human (fragment)

Species: Mus musculus (mouse)

Accession: AF040946

Query Match 28.9% (28.9% 17; DB 2; Length 12)

Best Local Similarity 44.1% (44.1% 17; DB 2; Length 12)

Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AVSR 4

DB 2 AVSR 5

RESULT 16

1 cell receptor alpha chain V region (V-9/10/1) human (fragment)

Species: Mus musculus (mouse)

Accession: AF040946

Query Match 28.9% (28.9% 17; DB 2; Length 12)

Best Local Similarity 44.1% (44.1% 17; DB 2; Length 12)

Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AVSR 4

DB 2 AVSR 5

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us-09-730-174a-5.closed.rsp

ALIGNMENTS

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us-09-730-174a-5.closed.rag

Sequence alignment of us-09-730-174a-5.closed.rag (with human parathyroid hormone)

Sequence alignment of us-09-730-174a-5.closed.rag

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US-08 428-257A-4
1  Sequence 4, Application 08/28/95, Ver 1.0
2  Patent No. 6037137
3  GENERAL INFORMATION:
4  APPLICANT: IBM PC compatible
5  OPERATING SYSTEM: PC-DOS/MS-DOS
6  CURRENT APPLICATION DATA:
7  FILING DATE: 07/26/95
8  CLASSIFICATION: 514
9  INFORMATION FOR SEQ ID NO: 14:
10  SEQUENCE CHARACTERISTICS:
11  LENGTH: 10 amino acids
12  TYPE: amino acid
13  TOPOLOGY: linear
14  MOLECULE TYPE: protein
15  US-08-428-257A-14

Query Match 42.4% Query 35, EP 2; Length 10;
Best Local Similarity 83.3% ID 1, No. 81;
Matches 5, Conservative 3, Identical 0, Gaps 0;

CV 2 VSPEL 7
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14 1 VSPEL 5

RESULT 7
US-08-802-981-124
1  Sequence 424, Application 08/23/95, Ver 1.0
2  Patent No. 6037137
3  GENERAL INFORMATION:
4  APPLICANT: Kometiya, Akira
5  OPERATING SYSTEM: PC-DOS/MS-DOS
6  CURRENT APPLICATION DATA:
7  FILING DATE: 20-FEB-1997
8  CLASSIFICATION: 435
9  ATTORNEY/AGENT INFORMATION:
10  NAME: Hunter, Tom
11  REGISTRATION NUMBER: 38,492
12  REFERENCE/DOCKET NUMBER: 610,65 00030005
13  TELECOMMUNICATION INFORMATION:
14  TELEPHONE: (415) 576-0200
15  TELEFAX: (415) 576-0300
16  INFORMATION FOR SEQ ID NO: 134:
17  SEQUENCE CHARACTERISTICS:
18  LENGTH: 11 amino acids
19  TYPE: amino acid
20  TOPOLOGY: linear
21  MOLECULE TYPE: peptide
22  FEATURE:
23  NAME/FEY: Modified site
24  LOCATION: 3
25  OTHER INFORMATION: /product: "Aib"
26  US-08-802-981-124

US-08 428-257A-4
1  Sequence 4, Application 08/28/95, Ver 1.0
2  Patent No. 6037137
3  GENERAL INFORMATION:
4  APPLICANT: IBM PC compatible
5  OPERATING SYSTEM: PC-DOS/MS-DOS
6  CURRENT APPLICATION DATA:
7  FILING DATE: 07/26/95
8  CLASSIFICATION: 514
9  INFORMATION FOR SEQ ID NO: 14:
10  SEQUENCE CHARACTERISTICS:
11  LENGTH: 10 amino acids
12  TYPE: amino acid
13  TOPOLOGY: linear
14  MOLECULE TYPE: protein
15  US-08-428-257A-14

Query Match 42.4% Query 35, EP 2; Length 10;
Best Local Similarity 83.3% ID 1, No. 81;
Matches 5, Conservative 3, Identical 0, Gaps 0;

CV 2 VSPEL 7
111111
14 1 VSPEL 5

RESULT 7
US-08-802-981-124
1  Sequence 424, Application 08/23/95, Ver 1.0
2  Patent No. 6037137
3  GENERAL INFORMATION:
4  APPLICANT: Kometiya, Akira
5  OPERATING SYSTEM: PC-DOS/MS-DOS
6  CURRENT APPLICATION DATA:
7  FILING DATE: 20-FEB-1997
8  CLASSIFICATION: 435
9  ATTORNEY/AGENT INFORMATION:
10  NAME: Hunter, Tom
11  REGISTRATION NUMBER: 38,492
12  REFERENCE/DOCKET NUMBER: 610,65 00030005
13  TELECOMMUNICATION INFORMATION:
14  TELEPHONE: (415) 576-0200
15  TELEFAX: (415) 576-0300
16  INFORMATION FOR SEQ ID NO: 134:
17  SEQUENCE CHARACTERISTICS:
18  LENGTH: 11 amino acids
19  TYPE: amino acid
20  TOPOLOGY: linear
21  MOLECULE TYPE: peptide
22  FEATURE:
23  NAME/FEY: Modified site
24  LOCATION: 3
25  OTHER INFORMATION: /product: "Aib"
26  US-08-802-981-124

```


NAME: FRANK, ROBERT T.
 REGISTRATION NUMBER: 22,174
 REFERENCE/DOCKET NUMBER: 09/06 0007
 TELECOMMUNICATION INFORMATION
 TELEPHONE: 404-817-5474
 TELEFAX: 404-817-3799
 IN EMAIL FOR SEQUENCE NO: 174
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 MOLECULE TYPE: peptide
 HYPOTHETICAL: no
 ANTI-SENSE: no
 US-09-817-547A-17

Query Match 40.7% Seq. No. 34; DB 3; Length 6;
 Best Local Similarity 100.0% Seq. No. 1,76+05;
 Mismatches 4; Conservative 0; Mismatches 0; Indels 0; Caps 0;

22 9 HNS 12
 14 1 HNS 4

RESULT 12
 US-09-817-547A-15
 : Sequence 15, Application US/09817615A
 : Patent No. 6040790
 : GENERAL INFORMATION:
 : APPLICANT: Adormann, Knut
 : APPLICANT: Beck, Dieter
 : APPLICANT: Maderlein, Markus
 : FILER OF INVENTION: Peptide from the hPTH Sequence
 : NUMBER OF SEQUENCES: 36
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Jones & Askew, LL
 : STREET: 191 Peachtree Street, 17th Floor
 : CITY: Atlanta
 : STATE: Georgia
 : COUNTRY: USA
 : ZIP: 30303
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: ECLIPSE/VS 108
 : SOFTWARE: Patent In Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09/09-1,547A
 : FILING DATE:
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: PCT/DE 92/03757
 : FILING DATE: 29 SEP 1994
 : ATTORNEY/AGENT INFORMATION:
 : NAME: FRUST, ROGER T.
 : REGISTRATION NUMBER: 22,174
 : REFERENCE/DOCKET NUMBER: 09/06 0007
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 404-818-3700
 : TELEFAX: 404-818-3799
 : IN EMAIL FOR SEQ. NO: 15
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 7 amino acids
 : TYPE: amino acid
 : STRANDEDNESS: unknown
 : MOLECULE TYPE: unknown
 : MOLECULE TYPE: peptide
 : HYPOTHETICAL: no
 : ANTI-SENSE: no
 : US-09-817-547A-15

Query Match 40.7% Seq. No. 34; DB 3; Length 7;
 Best Local Similarity 100.0% Seq. No. 1,76+05;
 Mismatches 4; Conservative 0; Mismatches 0; Indels 0; Caps 0;

22 9 HNS 12
 14 1 HNS 4

RESULT 14
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 : Sequence 64, Application US/09748021-64
 : Patent No. 5817752
 : GENERAL INFORMATION:
 : APPLICANT: YU, LIN
 : FILER OF INVENTION: CYCLOPEPTIDES COMBINING A


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: TELEX: 706141
: INFORMATION FOR GEN. 1 NO: 64:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURES:
: NAME/KEY: Mod11-1-s11
: LOCATION: 1
: OTHER INFORMATION: /GenBank "GHER"
: OTHER INFORMATION: /Jalview Hs
: OTHER INFORMATION: /Uniprot "HsGcrine"
US-09-730-174a-5

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Query Match 40.74% Score 24 DB 32 Length 33
Best Local Similarity 100.0% Posit No. 1.7e+05
Matches 4 Conservative 3 Gaps 0
Q7 9 HMDG 12
Db 2 HMDG 6

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Search completed: September 21, 2002, 1:09:33
Job time: 192 sec

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Condition	Control (%)	MCI (%)	AD (%)
1	95	75	35
2	90	65	25
3	95	70	30
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Age Group	Percentage of Respondents
18-29	~65%
30-49	~75%
50-69	~85%
70+	~90%

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RESULT 15

Q43929 PRELIMINARY: 1997 9 AA.
 A: Q43929; Q43929; Q43929; Q43929;
 D1 01 NOV 1996 (TREVINO L. L. Last sequence update)
 D1 01 JUN 2002 (TREVINO L. L. Last sequence update)
 DE GRA FOR EXP. (TREVINO L. L. (FRAGMENT))
 GN EXP.
 OS Aeromonas faecalis (Aeromonas faecalis).
 OC Bacteria: Proteobacteria: gamma subdivision: Aeromonadaceae;
 OC Aeromonas.
 OX NCBI_taxid: 648;
 RN 111
 RP SEQUENCE FROM N.A.
 RC STRAIN VARIANTS STRAINS:
 RX MEDLINE 97084747; JOMed 8435555;
 RA Kariyehov A.V., Moshchyn S.
 RT "Study of the intergenic xerC-xcrB region and its application as a
 RT simple preliminary test for Aeromonas spp."
 RL FEMS Microbiol. Lett. 147:195-197 (96).
 DR EMBL: X89444; CAA63431;
 DR EMBL: X89444; CAA63431;
 DR EMBL: X89444; CAA63431;
 DR EMBL: X89444; CAA63431;
 FT NON-TER 1 1
 SJ SEQUENCE 9 AA: 755 69444472B GR064;

Query Match

26.29; Score 14; DB 2; Length 9;

Best Local Similarity: 50.00; ID 1 No. 5,66,05;

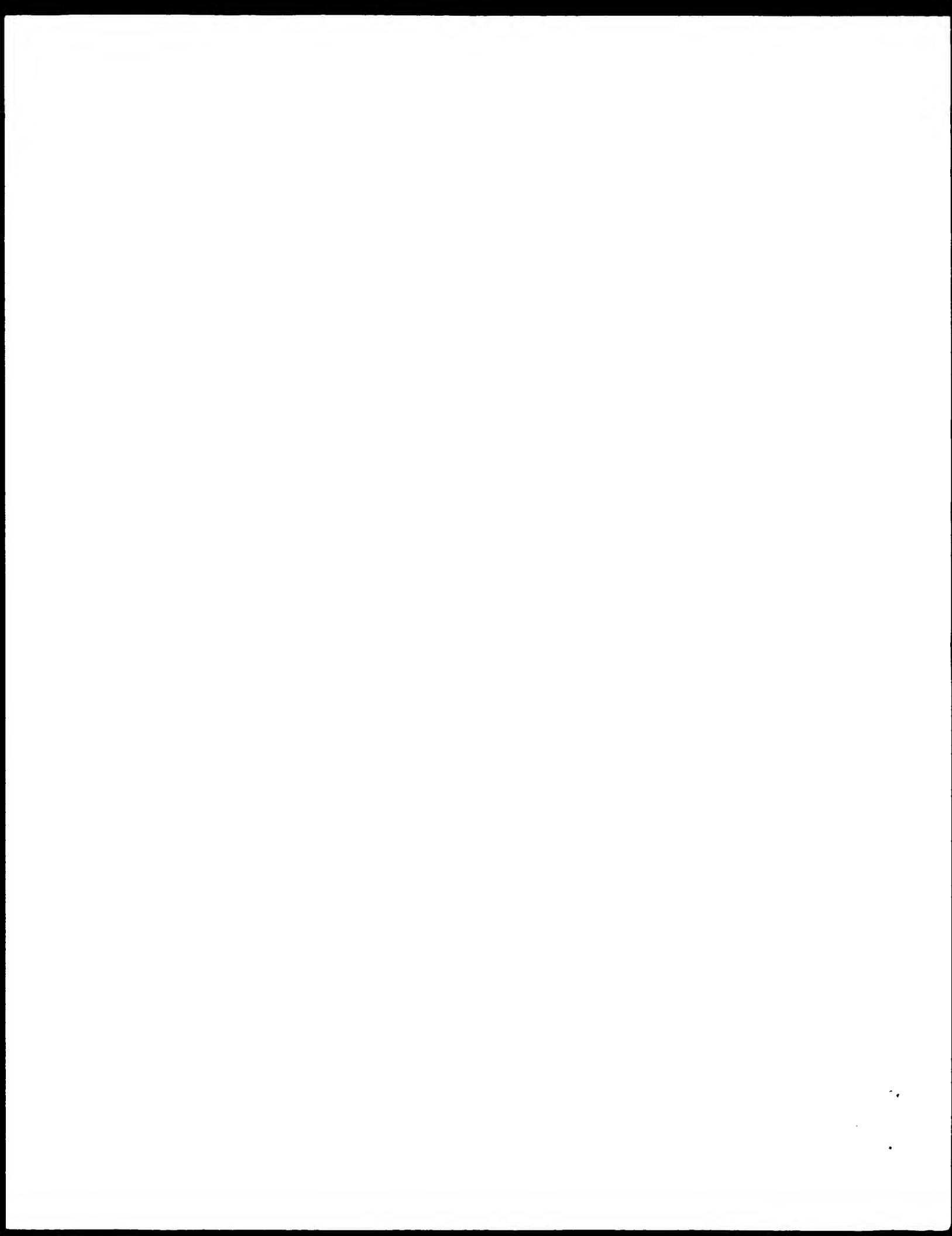
Matches 4; Conservative 1; Mismatches 1; Gaps 0;

QY 4 E:0FMNL 11

11 1 11

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Search completed: September 21, 2002. 11:09
 Job time: 708 sec



Protein		Sequence	Score	Match	Length	Identity	Similarity	Gap	Penalty	Score	Match	Length	Identity	Similarity	Gap	Penalty
Human parathyroid hormone	1-34	1-34	100.0	100.0	34	100.0	100.0	0	0.0	100.0	100.0	34	100.0	100.0	0	0.0
Rat parathyroid hormone	1-34	1-34	99.7	99.7	34	99.7	99.7	0	0.0	99.7	99.7	34	99.7	99.7	0	0.0
Human parathyroid hormone-related protein	1-34	1-34	99.5	99.5	34	99.5	99.5	0	0.0	99.5	99.5	34	99.5	99.5	0	0.0
Rat parathyroid hormone-related protein	1-34	1-34	99.3	99.3	34	99.3	99.3	0	0.0	99.3	99.3	34	99.3	99.3	0	0.0
Human parathyroid hormone-related protein	1-34	1-34	99.1	99.1	34	99.1	99.1	0	0.0	99.1	99.1	34	99.1	99.1	0	0.0
Rat parathyroid hormone-related protein	1-34	1-34	98.9	98.9	34	98.9	98.9	0	0.0	98.9	98.9	34	98.9	98.9	0	0.0
Human parathyroid hormone-related protein	1-34	1-34	98.7	98.7	34	98.7	98.7	0	0.0	98.7	98.7	34	98.7	98.7	0	0.0
Rat parathyroid hormone-related protein	1-34	1-34	98.5	98.5	34	98.5	98.5	0	0.0	98.5	98.5	34	98.5	98.5	0	0.0
Human parathyroid hormone-related protein	1-34	1-34	98.3	98.3	34	98.3	98.3	0	0.0	98.3	98.3	34	98.3	98.3	0	0.0
Rat parathyroid hormone-related protein	1-34	1-34	98.1	98.1	34	98.1	98.1	0	0.0	98.1	98.1	34	98.1	98.1	0	0.0
Human parathyroid hormone-related protein	1-34	1-34	97.9	97.9	34	97.9	97.9	0	0.0	97.9	97.9	34	97.9	97.9	0	0.0
Rat parathyroid hormone-related protein	1-34	1-34	97.7	97.7	34	97.7	97.7	0	0.0	97.7	97.7	34	97.7	97.7	0	0.0
Human parathyroid hormone-related protein	1-34	1-34	97.5	97.5	34	97.5	97.5	0	0.0	97.5	97.5	34	97.5	97.5	0	0.0
Rat parathyroid hormone-related protein	1-34	1-34	97.3	97.3	34	97.3	97.3	0	0.0	97.3	97.3	34	97.3	97.3	0	0.0
Human parathyroid hormone-related protein	1-34	1-34	97.1	97.1	34	97.1	97.1	0	0.0	97.1	97.1	34	97.1	97.1	0	0.0
Rat parathyroid hormone-related protein	1-34	1-34	96.9	96.9	34	96.9	96.9	0	0.0	96.9	96.9	34	96.9	96.9	0	0.0
Human parathyroid hormone-related protein	1-34	1-34	96.7	96.7	34	96.7	96.7	0	0.0	96.7	96.7	34	96.7	96.7	0	0.0
Rat parathyroid hormone-related protein	1-34	1-34	96.5	96.5	34	96.5	96.5	0	0.0	96.5	96.5	34	96.5	96.5	0	0.0
Human parathyroid hormone-related protein	1-34	1-34	96.3	96.3	34	96.3	96.3	0	0.0	96.3	96.3	34	96.3	96.3	0	0.0
Rat parathyroid hormone-related protein	1-34	1-34	96.1	96.1	34	96.1	96.1	0	0.0	96.1	96.1	34	96.1	96.1	0	0.0
Human parathyroid hormone-related protein	1-34	1-34	95.9	95.9	34	95.9	95.9	0	0.0	95.9	95.9	34	95.9	95.9	0	0.0
Rat parathyroid hormone-related protein	1-34	1-34	95.7	95.7	34	95.7	95.7	0	0.0	95.7	95.7	34	95.7	95.7	0	0.0
Human parathyroid hormone-related protein	1-34	1-34	95.5	95.5	34	95.5	95.5	0	0.0	95.5	95.5	34	95.5	95.5	0	0.0
Rat parathyroid hormone-related protein	1-34	1-34	95.3	95.3	34	95.3	95.3									

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Sequence 42, Application US/09484228
Patent No. 5968753
GENERAL INFORMATION
APPLICANT: Tseong-Law, Janet
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APPLICANT: Gutierrez, Roy
APPLICANT: Robinson, Sar A.
APPLICANT: Deans, Robert J.
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ATTORNEY/AGENT INFORMATION:
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APPLICANT: Robinson, Sar A.
APPLICANT: Deans, Robert J.
TITLE OF INVENTION: SELECTIVE RELEASE CELL
CLASSIFICATION: 435
NUMBER OF SEQUENCES: 215
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 09/09484228
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Guthrie, Janice
REGISTRATION NUMBER: 4357
ADDRESS: 1200 K Street, N.W.
TELEPHONE: (714) 440-6453

US 09-730-174A
Sequence 42, Application US/09484228
Patent No. 5968753
GENERAL INFORMATION
APPLICANT: Tseong-Law, Janet
APPLICANT: Kober, Joan A.
APPLICANT: Al-Aldaly, Fahad A.
APPLICANT: Gutierrez, Roy
APPLICANT: Robinson, Sar A.
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ADDRESS: 1200 K Street, N.W.
TELEPHONE: (714) 440-6453


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18  TYPE: amino acid
19  STRANDEDNESS: linear
20  FOLDING TYPE: linear
21  MODIFICATION TYPE: peptide
22  AMINO ACID SEQUENCE:
23  INFORMATION SOURCE:
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